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Query Match 100.

Best Local Similarity 100.

Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FRAGMENT TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                            100036
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE:
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RESULT 1
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Sequence 100, App
Sequence 99, Appl
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16, Appl
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Sequence 4, Appli
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                                                                                                                                                                                                                                                                                                                                                                          Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                   5, 2003, 09:46:51; Search time 9.85714 Seconds (without alignments) 26.864 Million cell updates/sec
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100,
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Sequence 10
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Sequence 8
Sequence 1
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/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PcTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/backfiles1.pep:*
         GenCore version 5.1.3 Copyright (c) 1993 - 2003 Compugen Ltd
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US-08-652-971-10
US-08-991-938A-10
US-08-911-93A-10
US-08-151-219-4
PCT-US94.13205-4
US-08-151-219-1
PCT-US94.13205-1
US-09-174-216-4
US-08-446-692-75
US-08-446-692-75
US-08-446-692-75
US-08-448-951A-75
US-08-488-951A-75
US-08-488-951A-75
US-08-98-98-951A-75
US-09-079-372-10
US-09-079-372-10
US-09-079-372-15
US-09-079-372-15
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US-08-446-692-99
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US-08-446-692-100
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US-08-488-351A-69
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-151-219-2
                                                                                                                                                                               262574 seqs, 29422922 residues
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                                                                                                                                                                                                                                                   Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                sw model
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Gapop 10.0 , Gapext 0.5
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                                                 protein search, using
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Maximum DB seq length: 200000000
                                                                                                          US-09-700-329-1
53
1 EGPWLEEEE 9
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Match Length
                                                                      February
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                                                                                                                      Perfect score:
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                                                                                                                                                                                 Searched:
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                                                                                                              Title:
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Sequence 7, Appli
Sequence 14, Appl
Sequence 2, Appli
Sequence 76, Appl
Sequence 76, Appl
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Sequence 2,
Sequence 2,
Sequence 2,
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Sequence
Sequence
                     Sequence
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Sequence 2, Application US/08151219

Sequence 2, Application US/08151219

Sequence 2, Application US/08151219

Sent No. 5468494

Sent No. 5468494

APPLICANT: Grimes, Philip C.

APPLICANT: Karr, Stephen

APPLICANT: Michaell, Dov.

APPLICANT: Michaell, Dov.

APPLICANT: Scibienski, Robert

TITLE OF INVENTION: IMPROVED IMMUNGGENIC COMPOSITIONS

TITLE OF INVENTION: AGAINST HUMAN GASTRIN 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 53; DB 1; Length 9; 100.0%; Pred. No. 2e+05; cive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Dimitrios T. Drivas, white and Case STREET: 1155 Avenue of the Americas CITY: New York COUNTRY: New York COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PatentIn Release #1.0, Version #1.25
US-08-488-351A-99
US-08-446-692-95
US-08-04-88-351A-95
US-09-079-372-7
US-09-079-372-14
US-09-446-692-76
US-08-446-692-76
US-08-488-351A-76
US-08-488-351A-76
US-08-488-351A-7
US-08-480-351B-3
US-08-480-221A-3
US-08-480-221A-3
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US-08-474-988B-7
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US-08-474-988B-2
US-08-394-442B-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/151,219
FILING DATE: 12-NOV-1993
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Drivas, Dimitrios T.
REGISTRATION NUMBER: 32,218
REFERENCE/DOCKET NUMBER: 1102865-028
TELECOMMNICATION:
                                                                                                                                                                                                                                                                                                                                          ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
DOBRATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (212) 819-8286
TELEFAX: (212) 354-8113
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 9 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: peptide HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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CORRESPONDENCE ADDRESS:
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Gaps

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ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT, LLP STREET: 4 Embarcadero Center, Suite 3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Cheng, Jill
APPLICANT: Lasky, Laurence A.
TITLE OF INVENTION: A NOVEL KAPPA/MU-LIKE PROTEIN TYROSINE
TITLE OF INVENTION: PHOSPHATASE, PTP LAMBDA
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 53; DB 2; Length 12; 100.0%; Pred. No. 0.0043;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                             ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURREW APPLICATION DATA:
APPLICATION NUMBER: US/08/652,971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
FILLING DATE: 17-DEC-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: A-63478-3/WHD/MIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
South San Francisco
California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/652,971
FILING DATE: 24-MAY-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 10, Application US/08991258A Patent No. 5928887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: P103
RELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 225-3216
TELEFAX: (415) 922-9881
TELEX: 910 371-7168
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Dreger, Ginger R.
REGISTRATION NUMBER: 33,055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Dreger, Walter H. REGISTRATION NUMBER: 24,190
                                                              United States
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGIH: 12 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: San Francisco
STATE: California
COUNTRY: United States
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Matches 9; Conservative
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CLASSIFICATION: 435
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CLASSIFICATION: 435
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                                                            COUNTRY: UR
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0
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APPLICANT: Grimes, Stephen
APPLICANT: Michaell, Dov
APPLICANT: Michaell, Dov
APPLICANT: Michaell, Dov
TITLE OF INVENTION: IMPROVED IMMUNOCENIC COMPOSITIONS
TITLE OF INVENTION: AGAINST HUMAN GASTRIN 17
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dimitrios T. Drivas, White and Case
STRRET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 10, Application US/08652971
Patent No. 5814507
GENERAL INFORMATION:
APPLICANT: Cheng, Jill
APPLICANT: Lasky, Laurence A.
TITLE OF INVENTION:
A NOVEL KAPPA/MU-LIKE PROTEIN TYROSINE
TITLE OF INVENTION: PHOSPHATASE, PTP LAMBDA
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSER: Generacch, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 5; Length 9;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/13205
FILING DATE: 12 NOV-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY AGENT INFORMATION:
NAME: Drivas, Dimitrios T.
REGISTRATION NUMBER: 32,218
REPERBUCE/DOCKET NUMBER: 1102865-028
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 33; 100.0%; Pred. No.
                                                                                                                                                        Sequence 2, Application PC/TUS9413205 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (212),819-8286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (212) 354 -8113 INFORMATION FOR SEQ ID NO: 2 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FRAGMENT TYPE: N-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 100.
Best Local Similarity 100.
Matches 9; Conservative
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: peptide HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 100036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          amino acid
GY: linear
            ECPWLEEEE 9
                                    PIPIPIPI
EGPWLEEEE 9
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                                                                                                                                   PCT-US94-13205-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Cheng, J111
APPLICANT: Lasky, Laurence A.
TITLE OF INVENTION: A NOYEL KAPPA/MU-LIKE PROTEIN TYROSINE
TITLE OF INVENTION: PHOSPHATASE, PTP LAMBDA
CORRESPONDENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 53; DB 2; Length 12; Pred. No. 0.0043; Mismatches 0; Indels
                                                                                                                                                                                                                                           Length 12;
                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: DATE: PATENT PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/769,399
                                                                                                                                                                                                                                      100.0%; Score 53; DB 2; L. 100.0%; Pred. No. 0.0043; tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd.
CITY: South San Francisco
STATE: California
COUNTRY: United States
                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 10, Application US/08769399
Patent No. 5976852
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P1033
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Dreger, Ginger R.
REGISTRATION NUMBER: 33,055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: P1
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                          INFORMATION FOR SEQ ID NO: 10:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (415) 225-3216
TELEFAX: (415) 952-9881
TELEX: 910 371-716
INFORMATION FOR SEQ ID NO: 10
                   TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.08
                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                          Query Match 100.

Best Local Similarity 100.

Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                    ; TOPOLOGY: linear
; MOLEGULE TYPE: protein
US-08-991-258A-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; MOLECULE TYPE: protein US-08-769-399-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                        1 EGPWLEEEE 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 EGPWLEEEE
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EGPWLEEEE
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                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-769-399-10
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                                                                                                                                                                                                                   ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT, LLP STREET: 4 Embarcadero Center, Suite 3400
STREET: Can Francisco
STATE: California
COUNTRY: United States
                                                                               APPLICANT: Cheng, Jill
APPLICANT: Lasky, Laurence A.
TITLE OF INVENTION: A NOVEL KAPPA/MU-LIKE PROTEIN TYROSINE
TITLE OF INVENTION: PHOSPHATASE, PTP LAMBDA
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 53; DB 3; Length 12; 100.0%; Pred. No. 0.0043; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 4, Application US/08151219
Patent No. 5468494
GENERAL INFORMATION:
APPLICANT: Gevas, Philip C.
APPLICANT: Karr, Stephen
APPLICANT: Michaell, Dov
APPLICANT: Michaell, Dov
TITLE OF INVENTION: IMPROVED IMMUNOGENIC COMPOSITIONS
TITLE OF INVENTION: AGAINST HUMAN GASTRIN 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/991,953A FILING DATE: 16-DEC-1997 CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3: Dimitrios T. Drivas, White and Case 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A-63478-3/WHD/MTK
                Sequence 10, Application US/08991953A Patent No. 6083748
                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Dreger, Walter H. REGISTRATION NUMBER: 24,190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: A-TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFHONE: (415) 781-1989
TELEFAX: (415) 398-3249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 24-MAY-1996 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                     Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 100.
Best Local Similarity 100.
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                  ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       amino acid
                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New York
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STREET: 11
US-08-991-953A-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-991-953A-10
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US-08-151-219-4
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TELEFAX: (212) 354-8113
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
US-08-151-219-1
                                                                                                                                                                                                                                                                                               ; FRAGMENT TYPE: N-terminal PCT-US94-13205-4
                                                                                                                                                                                                                                                                                                                                                                Ouery Match
Best Local Similarity 100..
                                                                                                   15 amino acids
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Best Local Similarity 100.
Matches 9; Conservative
                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS
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                                                                                                                                  amino acid
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TRY: U.S.A.
100036
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 EGPWLEEEE 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY:
                                                                                                      LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 9
US-08-151-219-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Gevas, Philip C.
APPLICANT: Grimes, Stephen
APPLICANT: Marr, Stephen
APPLICANT: Scibienski Robert
APPLICANT: Scibienski Robert
TITLE OF INVENTION: IPROVED IMMUNOGENIC COMPOSITIONS
TITLE OF INVENTION: AGAINST HUMAN GASTRIN 17
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                                            COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
PFILING DATE: 12-NOV-1993
CLASSIFICATION: 514
ATTORNEY AGENT INPORMATION:
NAME: DESIGN TO STANDER TO STAND
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ZIP: 100036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Dimitrios T. Drivas, White and Case STREET: 1155 Avenue of the Americas CITY: New York COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Drivas, Dimitrios T.
REGISTRATION NUMBER: 32,218
REFERENCE/DOCKET NUMBER: 1102865-028
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 819-8286
TELEFRA: (212) 354-8113
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Drivas, Dimitrios T.
REGISTRATION NUMBER: 32,218
REFERENCE/DOCKET NUMBER: 1102865-028
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 819-8286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: PCT/US94/13205
FILING DATE: 12-NOV-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; FRAGMENT TYPE: N-terminal US-08-151-219-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: peptide HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
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Best Local Similarity
Matches 9; Conserv
                           U.S.A.
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                           COUNTRY:
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SEQUENCE CHARACTERISTICS:

SEQUENCE CHARACTERISTICS:

LENGUR: anino acid

TYPE: anino acid

TYPE: anino acid

TYPE: anino acid

TYPE: anino acid

MATTORISTICATE: Peptide

ATTORISTICATE: Peptide

MATTORISTICATE: Peptide

MATTORISTICATE: Peptide

APPLICANT: Genes ATTORISTICATE: Peptide

APPLICANT: Genes ATTORISTICATE

ATTORISTICATION ANDRESS: ATTORISTICATION

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MOLECULE TYPE:
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US-08-446-692-75
LENGTH: 17
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                                                                                                          FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                 GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: GEVAS., Philip C.
APPLICANT: GATINES, Stephen
APPLICANT: Michaell, Dov.
APPLICANT: Michaell, Dov.
APPLICANT: Stephen
TITLE OF INVENTION: IMPROVED IMMUNGENIC COMPOSITIONS
TITLE OF INVENTION: AGAINST HUMAN GASTRIN 17
NUMBER OF SEQUENCES: S
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 53; DB 5; Length 16; 100.0%; Pred. No. 0.0059;
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Sequence 4, Application US/09174216A
Patent No. 6335176
GENERAL INFORMATION:
APPLICANT: Inglese, James
APPLICANT: GIICkman, Joseph Fraser
TITLE OF INVENTION: Incorporation of Phosphorylation Sites
FILE REFERENCE: 1073.050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                 ADDRESSEE: Dimitrios T. Drivas, White and Case STREET: 1155 Avenue of the Americas CITY: New York STATE: New York
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY AGENT INFORMATION:
NAME: Drivas, Dimitrios T.
REGISTRATION NUMBER: 32,218
REGISTRATION NUMBER: 1102865-028
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 819-8286
TELEPHONE: (212) 854-8113
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/174,216A CURRENT FILING DATE: 1998-10-16 NUMBER OF SEQ ID NOS: 8 SOFTWARE: Petentin Ver. 2.1 SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Vers
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/13205
FILING DATE: 12-NOV-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
TOPOLOGY: 1:-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FRAGMENT TYPE: N-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: peptide HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                        STATE: New York
COUNTRY: U.S.A. |
ZIP: 100036 |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best_Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 EGPWLEEEE 9
   1 EGPWLEEEE 9
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                                                                         RESULT 10
PCT-US94-13205-1
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TITLE OF INVENTION: Immunogenic LHRH peptide constructs
TITLE OF INVENTION: and synthetic universal immune stimulators for vaccines
UNUMBER OF SEQUENCES: 114
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                ;
0
                                        FEATURE: OTHER INFORMATION: Description of Artificial Sequence: Designed OTHER INFORMATION: peptide to act as kinase substrate
                                                                                                                                                                                                                       100.0%; Score 53; DB 4; Length 17; 100.0%; Pred. No. 0.0062; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/446,692
FILING DATE: 7-UN-1995
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88.9%; Pred. No. 0.014;
live 1; Mismatches (
                                                                                                                    NAME/KEY: MOD_RES
LOCATION: (1)
COTHER INFORMATION: PYRROLIDONE CARBOXYLIC ACID
US-09-174-216-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: US
ZIP: 10154-0053
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 75, Application US/08446692; Patent No. 5759551; GENERAL INFORMATION:
APPLICANT: Ladd, Anna APPLICANT: Wang, Chang Yi APPLICANT: Zamb, Timothy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REGISTRATION NUMBER: 29,323
REFERENCE/DOCKET NUMBER: 11:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Maria C.H. Lin
STREET: 345 Park Avenue
TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Maria C.H. Lin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (212)415-8745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (516)751-6849 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12 amino acids
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Best Local Similarity 100.۰
در 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8; Conservative
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EGPWLEEEE 9
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                          COUNTRY:
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US-08-488-351A-75
Sequence 75, Application US/08488351A
Patent No. 2843446
GENERAL INFORMATION:
APPLICANT: Ladd, Anna
APPLICANT: Zamb, Timothy
TITLE OF INVENTION: Immunogenic LHRH peptide constructs
TITLE OF INVENTION: and synthetic universal immune stimulators for vaccines NUMBER OF SEQUENCES: 114
CORRESPONDENCE ADDRESS:
ADDRESSEE: Maria C.H. Lin
STREET: 345 Park Avenue
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Ladd, Anna
APPLICANT: Wang, Chang Yi
APPLICANT: Wang, Chang Yi
TITLE OF INVENTION: Immunogenic LHRH peptide constructs
TITLE OF INVENTION: and synthetic universal immune stimulators for vaccines
NUMBER OF SEQUENCES: 114
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STATE: NEW TOIR
STATE: NEW COUNTRY: US
ZUDINTRY: US
ZUDINTRY: US
ZUDINTRY: US
ZUDINTRY: US
ZUDINTRY: TEMPER COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: TEM PC COMPATIBLE,
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN NOTA:
APPLICATION NUMBER: US/08/488,351A
FILING DATE: 7-UN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/446,692
FILING DATE: 7-UN-1995
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/29,275
FILING DATE: 7-UN-1995
CLASSIFICATION NUMBER: US 08/29,275
FILING DATE: 27-APR-1994
CLASSIFICATION NUMBER: US 08/057,166
FILING DATE: 27-APR-1992
CLASSIFICATION NUMBER: 121-APR-1992
CLASSIFICATION NUMBER: US 08/057,166
FILING DATE: 27-APR-1992
CLASSIFICATION NUMBER: 121-A146 US2
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 50; DB
Pred. No. 0.01.
1; Mismatches
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Patent No. 5759531
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (516)751-6849
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
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Best Local Similarity 88.9
Matches 8; Conservative
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MOLECULE TYPE: peptide
US-08-488-351A-75
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US-08-446-692-74
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0
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Pred. No. 0.02;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 7-JUN-1995
CLASSIFICATION: 424
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CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/446,692
FILING DATE: 7-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 08/229,275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSILLALALION: "A.Z.
ATTORNEY/AGENT INFORMATION:
NAME: MATIA C.H. Lin
REGISTRATION NUMBER: 29,323
REFRENCE/CDOCKET NUMBER: 1151
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)415-8745
TELEPHONE: (212)415-8745
TELEPHONE: (215)751-6849
INFORMATION FOR SED ID NO: 74:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 anino acids
Lin
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88.9%;
ADDRESSEE: Maria C.H. Li
STREET: 345 Park Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ouery Match
Best Local Similarity 88.2
8; Conservative
                                                                                                                                                                             ZIP: 10154-0053
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy o
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                                                                      New York
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94.3%; Score 50; DB 2; Length 17;

Best Local Similarity 88.9%; Pred. No. 0.02;

Matches 8; Conservative 1; Mismatches 0; Indels
FILING DATE: 14-APR-1994
CLASSIPICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/057,166
FILING DATE: 27-APR-1992
CLASSIPICATION: 424
ATTORNEY AGENT INFORMATION:
NAME: Maria C.H. Lin
REGISTRATION NUMBER: 1151-4146 US2
FEFFENCE/DOCKET NUMBER: 1151-4146 US2
TELEPHONE: (212)415-8745
TELEPHONE: (216)751-6849
TELEPHONE: (217)751-6849
TELEPHONE: (217)751-6849
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TELEPHONE: TELEPHONE: (217)751-6849
TELEPHONE: TELEPHONE: (217)751-6849
TELEPHONE: TELE
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February 5, 2003, 09:40:45; Search time 26.5714 Seconds (without alignments) , 45.133 Million cell updates/sec
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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                              Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                          908470 segs, 133250620 residues
                                                                                OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                               BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                        Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                               US-09-700-329-1
53
1 EGPWLEEEE 9
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                                                                                                                                                                                                                    Perfect score:
                                                                                                                                                                                                                                            Sequence:
                                                                                                                                                                                                                                                                                                                                             Searched:
                                                                                                                        Run on:
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Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries Databas

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Anti-gastrin-17 im Human gastrin-617 im Antigastrin-617 im Antigenic peptide Human gastrin 17 a Human gastrin 17 a Human beptadecagas Gastrin fragment a Carboxy amidated g Human Janus kinase
SUMMARIES	AAV24399 AAX51205 AAX59434 AAAX6245 AAR74297 AAR74295 AAR49309 AAW45184 AAW43184
	221 118 127 127 128
% Query Match Length DB	9 9 112 115 116 117 117
% Query Match	10000000000000000000000000000000000000
Score	
Result No.	10849991

Grimes S, Karr SL, Michaeli D, Watson SA;

Gevas PC,

opposition of the property of the position of the property of	Tyrosine kinase su Gastrin hapten. H Arabidopsis transc Antigenic peptide Arabidopsis thalia Human DITHP polype
22 AAB91246 22 AAB59273 28 AAU76504 15 AAR762740 15 AAR62739 22 AAR72381 22 AAX72381 22 AAX72381 22 AAX72383 22 AAX72384 22 AAX72386 22 AAX72386 22 AAX72386 22 AAX72386 22 AAX72386 23 AAX72379 23 AAX72378 23 AAY72378 23 AAY72378 23 AAY72378 23 AAY72378 23 AAY72378	21 AAB13767 15 AAR62741 11 AAR06249 20 AAY05831 23 ABG60002 22 AAU16252
1000 1000 1000 1000 1000 1000	
11111 00000000000000000000000000000000	90. 84. 83. 77. 75.
11113111331113311133133333333333333333	

## ALIGNMENTS

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/note= "Glu modified by a peptide spacer conjugated to
    a diphtheria toxoid"
                                                                                      Glycine-extended gastrin-17; gastrointestinal tumour; immunogen; colorectal adenocarcinoma; antibody; progastrin; cholecystochinin B; anti-gastrin-17; anti-G-17.
                                                                                                                                    Location/Qualifiers
9
                AAW24399 standard; peptide; 9 AA.
                                                                                                                                                                                                                         97WO-US02029.
                                                                                                                                                                                                                                           96US-0011411.
                                                    (first entry)
                                                                      Anti-gastrin-17 immunogen.
                                                                                                                                                                                                                                                            (APHI-) APHTON CORP.
                                                                                                                                           Key
Modified-site
                                                                                                                                                                                      W09728821-A1.
                                                                                                                         Homo sapiens
                                                                                                                                                                                                                        07-FEB-1997;
                                                                                                                                                                                                                                           08-FEB-1996;
                                                    13-MAR-1998
                                                                                                                                                                                                       14-AUG-1997.
                                   AAW24399;
RESULT 1
         AAW24399
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Rattus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gevas PC,
                                                                                                                                                                                                                                                           AAY59434;
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                                                                  Sequence
                                                                                           Query Match
                                                                                                                                            Н
                                                                                                                                                                                                                    AAY59434
                                                                                                                                                                                                           RESULT
  SSSSXS
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                                                                                                   The present sequence represents a specific example of an anti-gastrin-17 inmunogen, comprising the N-terminal 9 amino acids of gastrin-17 conjugated to an immunogenic carrier such as Diphtheria toxoid, by a spacer peptide. This immunogenic composition is used in a new treatment of glycine-extended gastrin-17 (G17-G1y)-dependent gastrointestinal tumnours. Anti-G17 immunogenic composition is used in a new treatment tumnours. Anti-G17 immunogens raise antibodies which bind both the amidated and glycine-extended forms of G17. Neutralisation of progastrin G17-G1y prohormone by the antibodies inhibits the growth of tumour cells dependent on progastrin G17-G1y as growth stimulator or inducer. The method is especially for the treatment of colorectal adenocarcinomas in humans. The novel method is non-invasive, selectively reversible, does not damage normal tissue, does not require frequent repeated treatments and does not cross the blood brain barrier.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Immunogenic; treatment; hypergastrinemia; gastrin G17; gastrin G34; / pernicious anemia; anti-ulcer; proton pump inhibitor; colorectal diséase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This invention describes a novel mathod for the treatment or preventing hypergastrinemia by administering to a patient a gastrin G17 and/or G34 peptide fragment linked by an amino acid spacer to an immunogenic carrier. The methods are used to treat hypergastrinemic patients, particularly those with pernicious anemia, those receiving treatment with anti-ulcer agents such as proton pump inhibitors (particularly
                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Treating or preventing hypergastrinemia comprising administration of, e.g. anti-gastrin antibodies -
                          Treatment of glycine-extended gastrin-17-dependent gastrointestinal tumours - using anti-617 immunogenic composition, especially for
                                                                                                                                                                                                                                                                                                                                     0
                                                                                                                                                                                                                                                                                                            Length 9;
                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Watson
                                                                                                                                                                                                                                                                                                         Score 53; DB 18;
Pred. No. 7.8e+05;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human gastrin aminoterminal (1-9) G17 peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Michaeli D,
                                                   treatment of colorectal adenocarcinomas
                                                                             Example 1; Figure 1C; 37pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 11; 44pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY51305 standard; peptide; 9 AA.
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                                                                                                                                                                                                                                                                                                            100.0%;
100.0%;
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                                                                                                                                                                                                                                                                                               Ouery Match
Best Local·Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Grimes S,
WPI; 1997-415075/38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (APHT-) APHTON CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2000-116301/10.
                                                                                                                                                                                                                                                                                                                                                            1 EGPWLEEEE 9
                                                                                                                                                                                                                                                                                   9 AA;
                                                                                                                                                                                                                                                                                                                                                                             1 EGPWLEEEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
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                                                                                                                                                                                                                                                                                    Seguence
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ID AAY
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                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                  t
omeprazole or lansoprazole) or H_2 receptor blocking agents or antagonists, or those having colorectal disorders or diseases. T sequence represents the human gastrin G17 peptide which is used illustrate the method of the invention.
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                                                                                                                                                                            Length 9;
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                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tumour; tumour growth factor;
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                                                                                                                                                                            100.0%; Score 53; DB 21; 100.0%; Pred. No. 7.8e+05;
                                                                                                                                                                                                                               Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY59434 standard; peptide; 9 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Antigastrin-G17 immunogen.
                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              over chemotherapy alone.
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Matches 9; Conserv
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                                                                                                                               AA;
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EGPWLEEEE
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AAR74295 and AAR74297 are human gastrin 17 (hG17) antigenic peptides, used to produce anti-hG17 antibodies (Abs). The Abs can be induced in a patient, or used for passive immunisation, for the treatment of diseases in which hG17 is involved, e.g. gastric and duodenal ulceration; gastro-oesophageal reflux disease and cancer.
                                                             Immunogenic compsn. for producing anti-human gastrin 17 antibodies - used for treating e.g. gastro-oesophageal reflux disease, gastric and duodenal ulceration or cancer.
                                                                                                         Example 1; Page 3; 17pp; English.
                          Grimes S,
     (APHT-) APHTON CORP
                                             WPI; 1995-194034/25
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic
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                          Gevas PC,
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                                                                                                                                                                                            Sequence
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                                                                                                                                                                                                                                                                                               Immunogens against gastrin peptide(s) - used to induce antibodies that specifically neutralise single form of gastrin, G17 or \rm G34
                                                                                       of
                                                                                                                    Gastrin; tumours; peptic ulcers; diptheria toxoid; tetanus toxin;
                                                                                     Antigenic peptide fragment selected from the 12 N-terminal AAs heptadecagastrin (G17).
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                                                                                                                                                                                                                                                                                                                                               Antigenic fragments may be attached to an immunogenic carrier and used to raise Abs to a specific single form of Gastrin ie. GI7 or G34. Peptide fragments capable of binding to these Abs are useful in neutralising anti-gastrin Abs in vivo.
                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 53; DB 11; Length 12; 100.0%; Pred. No. 0.023; ative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human gastrin 17 antigenic peptide hG17(1-9)-Arg9.
                                                                                                                                                                                                                                                       Littenberg RL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAR74297 standard; peptide; 15 AA.
                         AAR06245 standard; peptide; 12 AA:
                                                                                                                                                                                                                                                                                                                            Claim 6; Page 19; 32pp; English.
                                                                                                                                                                                                                                                       Karr SL,
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89US-0301353
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                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                     (APHT-) APHTON CORP
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Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                 12 AA;
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24-JAN-1989;
                                                                     07-DEC-1990
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                                                                                                                                                                                                                                                         Gevas PC,
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                                                  AAR06245;
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                     AAR06245
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                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Immunogenic compsn. for producing anti-human gastrin 17 antibodies - used for treating e.g. gastro-oesophageal reflux disease, gastric
                                                                                                                                                                                                                                                                                                                                                                                                                                        Human gastrin 17; antigenic peptide hG17(1-9)-Ser9; immunisation; treatment; gastro-oesophageal reflux disease; gastric; duodenal; ulceration; cancer.
                                                                                ..
                                 100.0%; Score 53; DB 16; Length 15; 100.0%; Pred. No. 0.029;
                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Scibienski
                                                                                                                                                                                                                                                                                                                                                                                                    Human gastrin 17 antigenic peptide hG17(1-9)-Ser9.
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                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and duodenal ulceration or cancer.
                                                                                                                                                                                                                                                                               AAR74295 standard; peptide; 16 AA.
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                                                                                     Conservative
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                    Query Match
Best Local Similarity
7, Conserve
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15 AA;
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1 EGPWLEEEE
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RESULT 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to the treatment of gastroesophageal reflux disease (GERD) that comprises administering to a patient an immunogenic composition which generates anti-gastrin antibodies, which bind to proton pump inhibitor: The method provides a more effective method for controlling acid output by the stomach. The therapy is less costly. High gastrin levels associated with standard therapies are neutralized and undesirable side effects are reduced. The method permits a reduced dosage of acid reducing agent both at the acid producing level as well as the coil production stimulating level (gastrin). Reduction of dosages is desirable for prolonged treatment of GERD. In a combination therapy with L2 agonists or proton pump inhibitors, anti-gastrin 17 antibody titers can be maintenined by occasional bodster shots while gastric acid inhibitor dosing is reduced. Immunization allows a sufficient time for the esophagitis to completely heal and no surgery is required. The
                                                 0
                                                                                                                                                                                                                                                                                                                          Gastroesophageal reflux disease; GERD; gastrin; anti-gastrin antibody; histamine H_2; proton pump inhibitor; acid output; stomach; therapy; esophagitis; immunogen; human; heptadecagastrin; immunomimic; G17.
                                                                                                                                                                                                                                                                                             Human heptadecagastrin (G17) immunomimic with carboxy terminal spacer.
                                                   Gaps
                                                 ·;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Method for treatment of gastroesophageal reflux disease (GERD)
                  Length 16;
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                                                 0; Indels
                  Score 53; DB 16;
Pred. No. 0.031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "carboxy-terminal spacer"
                                                   Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /label= pglu
/note= "pyroglutamate"
10..16
/note= "carboxy-termin
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               100.0%;
ilarity 100.0%;
Conservative 0.
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Query Match
Best Local Similarity
'.~ 9; Conserv?
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                                                                                                   1 EGPWLEEEE 9
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Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                           Synthetic.
Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-MAY-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to the obtaining of a potent agonist or antagonist peptide by the replacement of selected amino acids with synthetic achiral amino acids. The present sequence represents a gastrin fragment analogue, where at least one of Tyrl2 and Phel7 is intended to be replaced by N benzylglycine. N-cyclohexylmethylglycine or the ring substituted derivatives thereof.
                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                 Bradykinin; N-benzylglycine; agonist; receptor study; antagonist; achiral; analgesic; angiotensin II; gastrin.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New bradykinin analogues contg. N-benzyl-glycine - useful as
bradykinin agonists or antagonists, useful e.g. as analgesics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 100.0%; Score 53; DB 17; Length 17; Best Local Similarity 100.0%; Pred. No. 0.033; Matches 9; Conservative 0; Mismatches 0; Indels
. No. 0.031;
                 Pred. No. 0.(
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "Pyroglutamic acid"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "C-terminal amide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Columns 7-8; 15pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
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                                                                                                                                                                                                                   AAW65184 standard; peptide; 17 AA.
  100.08; Pit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW24398 standard; peptide; 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             89US-0376839.
92US-0945664.
94US-0335202.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         94US-0335202
                                                                                                                                                                                                                                                                                                                                            Gastrin fragment analogue.
                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (REGC ) UNIV CALIFORNIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note-
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               Best Local Similarity
Matches 9; Conserv
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                                                                           EGPWLEEEE 9
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EGPWLEEEE 9
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EGPWLEEEE
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Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         07-NOV-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-SEP-1992;
07-NOV-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  07-JUL-1989;
                                                                                                                                                                                                                                                                                                   02-0CT-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US5527882-A
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic
                                                                                                                                                                                                                                                          AAW65184;
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Synthetic

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The present sequence represents carboxy-amidated gastrin-17. Treatment of gastrin-17-dependent gastrointestinal tumours comprises administering to a mammal an anti-gastrin 17 (G17) immunogenic composition. Anti-G17 immunogens raise antibodies which bind both the amidated and glycine-extended forms of G17. Neutralisation of progastrin G17-G1y prohormone by the antibodies inhibits the growth of tumour cells dependent on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              progastrin G17-G1y as growth stímulator or inducer. The method is especially for the treatment of colorectal adenocarcinomas in humans. This novel method is non-invasive, selectively reversible, does not
                                                           carboxy-amidated gastrin-17; gastrointestinal tumour; immunogen;
colorectal adenocarcinoma; antibody; progastrin; cholecystochinin B.
anti-gastrin-17; anti-G-17.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Treatment of glycine-extended gastrin-17-dependent gastrointestinal tumours - using anti-G17 immunogenic composition, especially for treatment of colorectal adenocarcinomas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           damage normal tissue, does not require frequent repeated treatments and does not cross the blood brain barrier.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Janus kinase 3; JAK/STAT inhibitor; peptide substrate; signal transducer and activator of transcription; osteoarthritis; degenerative joint disease; rheumatoid arthritis; leprosy; asthma; cancer; tumour; leukaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human Janus kinase 3 (JAK3) biotinylated peptide substrate GAS1.
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                                                                                                                                                                                                                                                                                                                                                                                     Watson SA;
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                                                                                                                                                                                                 /note= "C-terminal amide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 1; Figure 1B; 37pp; English.
                                                                                                                                                                  Location/Qualifiers
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                                                                                                                                                                                                                                                                                        97WO-US02029.
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                                            Carboxy-amidated gastrin-1
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            13-MAR-1998 (first entry
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                                                                                                                                                                                                                                                                                                                                                                                   Grimes S,
                                                                                                                                                                                                                                                                                                                                                     (APHT-) APHTON CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1997-415075/38.
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Matches 9; Conserv
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                                                                                                                                                                                 Modified-site
                                                                                                                                                                                                                                                                                        07-FEB-1997;
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                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                               WO9728821-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
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The sequence represents a synthetic biotinylated peptide substrate for human Janus kinase 3 (JAK3). The invention relates to the use of JAK57ATA (Janus kinase/signal transducer and activator of transcription) inhibitors other than debromchymenialdisine (DBH) and hymenialdisine (H) for inhibiting the progression or the likelihood of developing diseases involving cartilage degradation, and for requiating the expression or the likelihood of the expression of pro-inflammatory agents or cytokines in a chondrocyte, and cartilage degrading enzymes in a cell. A JAK3/STAT inhibitor of the invention is useful for inhibiting progression or likelihood of developing osteoarthritis or rheumatoid arthritis. The inhibitor is also useful for treating other JAK/STAT-mediated discases or disorders, including T cell-mediated disorders include human T cell-mediated disorders include human T cell-mediated disorders include human T cell eleukaemia/lymphoma virus (HTLV)-1, Sdzory's syndrome, c-abl transformation, natural killer-like T cell lymphomas (NK-like tumours) and graft-vs-host disease; cytokine hypersensitivity disorders include cute lymphocytic and lymphoplastic cleukaemias and lymphomas include acute lymphocytic and lymphoblastic leukaemias and lymphomas acute lymphocytic and lymphoblastic cleukaemias, B cell lymphomas and leukaemias of myeloid origin. DBH and H is the paper of the content in which JAK3 plays a role of the content in the infile the content in which JAK3 plays a role
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Use of inhibitors of Janus kinase/signal transducers and activators of transcription for inhibiting onset and progression of degenerative joint diseases or disorders such as osteoarthritis, rheumatoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       are useful as therapeutic agents in cancers in whic
in the initiation or progression of tumourigenesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
100.0%; Score 53; DB 22;
Best Local Similarity 100.0%; Pred. No. 0.033;
Matches 9; Conservative 0; Mismatches 0;
                                                                            "Glu is biotinylated"
                                                                                                                    amidated"
                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 6; Page 18; 55pp; English.
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AAB91246
ID AAB91246 standard; Peptide; 17 AA
XX
AC AAB91246;
XX
DT 22-JUN-2001 (first entry)
XX
                                                                                                                  "Phe is
                                                                                                                                                                                                                                                                            24-JAN-2000; 2000US-0177872.
28-NOV-2000; 2000US-0723490.
                                                                                                                                                                                                                                    22-JAN-2001; 2001WO-US02033
                                                                                                                    /note=
                                                                            /note=
                                                                                                                                                                                                                                                                                                                                        (GENZ ) GENZYME CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-465338/50.
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                                                      Modified-site
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                                                                                                                                                                                               26-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                             Vasios G;
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Gaps

Kauvar LM;

Cairns N,

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The present invention relates to detecting addition or removal of a phosphate group to or from a substrate. The method involves contacting a luminescent peptide with a binding partner that binds specifically to a phosphorylated peptide without regard to the particular amino acid sequence of the peptide. The method is useful for detecting phosphorylation and dephosphorylation modifications of proteins, including kinases and phosphatases. The methods can be used to study the kinase activity of different receptors e.g. the insulin receptor and to find agonists and antagonists of these receptors.
                                                                                                                                                                                                                                                                                                                                                                Assay for detecting phosphorylation and dephosphorylation modification of proteins by contacting luminescence peptide with a binding partner and measuring change in luminescence polarization .
                                                                                                                                                                                                                                                                                   Lee SK,
                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 70; Page 70; 89pp; English.
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                                                                                                                                                            99US-0138438.
99US-0349733.
                                                                                                                                            99US-0138311.
                                                                                                    2000WO-US16025
                                                                                                                                                                                                     28-APR-2000; 2000US-0200594
                                                                                                                                                                                                                                                                                   Sportsman JR, Hoekstra MF,
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                                                                                                                                                                                                                                              (LJLB-) LJL BIOSYSTEMS INC
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Matches 9; Conservative
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Modified-site
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                                                                                                                                            09-JUN-1999;
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                                                                                                                                                                                   08-JUL-1999;
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                                                             14-DEC-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention describes a modified therapeutic peptide (I) comprising a therapeutically active amino acid region (III) and a reactive group (II) (e.g., succinimidy1 and malelimido groups) attached to a less therapeutically active amino acid region (IV), which covalently bonds with amino/hydroxyl/thiol groups on blood components to form a peptidase stabilised therapeutic peptide composed of 3-50 amino acids. (I) are useful for modifying therapeutic peptides e.g. hormones, growth factors and neurotransmitters, to protect them from peptidase activity in vivo for the treatment of various disorders. Endogenous therapeutic peptides are not suitable as drug candidates as they require frequent administration due to rapid degradation by peptidases in the body
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Modifying and attaching therapeutic peptides to albumin prevents peptidase degradation, useful for increasing length of in vivo activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Modifying and attaching therapeutic peptides to albumin prevents or reduces the action of peptidases to increase length of activity (half life) and specificity as bonding to large molecules decreases | intracellular uptake and interference with physiological processes.

AAB90829 to AAB92441 represent peptides which can be used in the exemplification of the present invention.
                                       Protection, endogenous therapeutic peptide, peptidase, conjugation; blood component, modification; succinimidy1; maleimido group, amino; hydroxy1; thiol; hormone; growth factor; neurotransmitter.
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Pred. No. 0.033;
Gastrin releasing peptide (GRP) SEQ ID NO:422.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 336; 733pp; English.
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99US-0153406.
99US-0159783.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-112059/12.
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Best Local Similarity
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                                                                                                                       Homo sapiens
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10-SEP-1999;
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                                                                                                                                            Synthetic.
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Gaps
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 DB 22; Length 17; 0.033;
                             0; Indels
Score 53; DB Pred. No. 0.03 Mismatches
                                                                                                                                                                                                                                                                                                                                                                         /note= "Pyroglutamic acid"
                                                                                                                                                                                                                                           Protein kinase A (PKA) substrate #3
                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                           AA.
                                                                                                                                                                                                                                                                       Protein kinase A; phosphorylation
                            0;
                                                                                                                                                        AAU76504 standard; peptide; 17
 100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98US-0174216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (PHAR-) PHARMACOPEIA INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-OCT-1998;
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Unidentified

AAB59273;

RESULT 12 AAB59273

Op

Matches

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The invention relates to a reagent (I) for incorporation of a phosphorylation site by reaction with a reactive side chain of a compound to be phosphorylated. (I) comparises a structure A-B-C, where A is a moiety that is specifically reactive with a reactive side chain, C is a peptide sequence comprising kinase substrate, and B is a linking moiety selected from any one of the 19 compounds given in the specification e.g. N-gamma-maleimidobutyrylory-succinamide ester. (I) is useful for phosphorylation, by reacting (I) with a compound to be phosphorylated comprising a protein kinase under phosphorylating the resulting production in assays such as drug discovery. The method is suitable for radioactively phosphorylating already synthesised proteins, without the need to carry out recombinant methods to incorporate an amino acid sequence. The method is highly adaptable and can be used to phosphorylate or according that contain reactive site groups. (I) avoids production of proteins having an inaccessible kinase substrate sequence as can result from known recombinant methods. Introduction of capenates in proteins is possible merely by increasing the ratio of reagent to protein, and the method allows labeled increasing the ratio of reagent to protein sites in protein's function or become phosphorylating does not interfere with the protein's function or become conduction of reagent to protein, and the method allows labeled conducts to be obtained that have a higher specific activity that is commally obtained with recombinant methods. The present sequence conduction with recombinant methods. The present sequence conduction of the invention. The protein sequence conduction of protein folding. The method allows is conducted to protein sequence conduction of protein folding. The method allows have been accombinant methods. The present sequence conduction of the invention. The protein sequence conduction of protein folding. The method in examples that demonstrate the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Glycine-extended gastrin-17; gastrointestinal tumour; immunogen; colorectal adenocarcinoma; antibody; progastrin; cholecystokinin B; anti-gastrin-17; anti-617.
                                                                                                          Reagent for phosphorylating a compound, comprises a moiety that is specifically reactive with reactive site chain of the compound, a linking moiety and a peptide sequence comprising kinase substrate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 53; DB 23; Length 17; 100.0%; Pred. No. 0.033; 1ive 0; Mismatches 0; Indels
                                                                                                                                                                                                      Disclosure; Column 8; 26pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW24397 standard; peptide; 18 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Glycine-extended gastrin-17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  96US-0011411.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12-MAR-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                  Glickman JF;
                                                               WPI; 2002-194620/25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 EGPWLEEEE 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EGPWLEEEE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14-AUG-1997
                     Inglese J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
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The present sequence represents glycine-extended gastrin-17. Treatment of glycine-extended gastrin-17 (Gl7-Gly)-dependent gastrointestinal tumours comprises administering an anti-gastrin 17 (anti-Gl7) immunogenic comprises administering an anti-gastrin 17 (anti-Gl7) immunogenic comprosition. Anti-Gl7 immunogens raise antibodies which bind both the amidated and glycine-extended forms of Gl7. Neutralisation of progastrin Gl7-Gly prohormone by the antibodies inhibits the growth of tumour cells dependent on progastrin Gl7-Gly as growth stimulator or adenocarcinomas. In humans. This novel method is non-invasive, selectively reversible, does not damage normal tissue, does not require frequent repeated treatments and does not cross the blood brain
                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Helper T cell epitope; universal immune stimulator; invasin; hapten;
                                                                              Treatment of glycine-extended gastrin-17-dependent gastrointestinal tumours - using anti-G17 immunogenic composition, especially for treatment of colorectal adenocarcinomas
                                                                                                                                                                                                                                                                                                                                                                                                        .,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Immunogenic luteinising hormone releasing hormone peptide(s) that suppress LHRH activity in males and females
                                                                                                                                                                                                                                                                                                                                                                              Length 18;
                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                            Watson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gastrin; peptic ulcers; gastrin-stimulated tumours.
                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 53; DB 18; 100.0%; Pred. No. 0.035;
                           Michaeli D,
                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claims 27, 37; Page 96; 213pp; English
                                                                                                                                      Example 1; Figure 1A; 37pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAR62740 standard; peptide; 12 AA.
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                          Karr SL,
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                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-SEP-1995 (first entry)
(APHT-) APHTON CORP.
                                                    WPI; 1997-415075/38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1994-357910/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ladd AE, Wang CY,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (LADD/) LADD A E.
(WANG/) WANG C Y.
(ZAMB/) ZAMB T.
                                                                                                                                                                                                                                                                                                                                                18 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                 σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                ||||||||||||
EGPWLEEEE
                                                                                                                                                                                                                                                                                                                                                                                                                                 1 EGPWLEEEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gastrin hapten.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28-APR-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO9425060-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10-NOV-1994
                          PC,
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                                                                                                                                                                                                                                                                                                                                                 Sequence
                          Gevas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 15
AAR62740
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Synthetic immunogenic peptides are provided in which a universal immune stimulator is linked to a peptide or protein hapten containing B cell and/or cytotoxic T lymphocyte epitopes, giving a product which causes potent immune responses to the coupled peptide or protein. The stimulator consists of (A) a promiscuous helper T cell epitope (Th) which elicits an immune response to the coupled peptide in members of a heterogeneous population expressing diverse HLA phenotypes, and (B) an adjuvant peptide sequence from the invasin protein of Yersinia. Spacer amino acid sequence from the invasin protein of Yersinia. Components. When the hapten is LHRH, then optionally the invasin domain can be omitted from the immune stimulator component.

The present sequence is an example of a gastrin hapten which can be bound to the immune stimulater furmours.
                                                                                                                                                                                                                                                                                                                                                                                                                   12 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                           Sednence
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Search completed: February 5, 2003, 09:47:56 Job time : 27.5714 secs 1 EGPWLEEEE 9 Op ò

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Gaps ó;

94.3%; Score 50; DB 15; Length 12; 88.9%; Pred. No. 0.071; tive 1; Mismatches 0; Indels

Query Match
Best Local Similarity 88.9 Matches 8; Conservative

0

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Pebruary 5, 2003, 09:49:21 ; Search time 6.85714 Seconds
(without alignments)
29.097 Million cell updates/sec
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1: /cgn2_6/ptodata/2/pubpaa/USO8_NEW_PUB.pep:*

2: /cgn2_6/ptodata/2/pubpaa/USO8_NEW_PUB.pep:*

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4: /cgn2_6/ptodata/2/pubpaa/USO6_PUBCOMB.pep:*

5: /cgn2_6/ptodata/2/pubpaa/USO7_NEW_PUB.pep:*

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14: /cgn2_6/ptodata/2/pubpaa/USO0_PUBCOMB.pep:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               129505
GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       129505 seqs, 22169297 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                              using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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53
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                                                                                                                 OM protein - protein search,
                                                                                                                                                                                                                                                                                  Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                   Scoring table:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Searched:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

		pli	, Ap	pp1	pli	Appl	pli	pli	ppli	Appli	ppli	Appli	Appli	Appl	Appl	ppl	ppli	ppl	Appl	Appl
	Description	Sequence 4, Appli	Sequence 1205, Ap	Sequence 16, App.	Sequence 4, Appl		7	Sequence 4, Appl	Sequence 8, A	Sequence 8, A	Sequence 4, A	Sequence 5, A	Sequence 6, A	Sequence 13,	Sequence 14,	Sequence 34, A	Sequence 7, A	Sequence 26, A	Sequence 18, A	Sequence 20, A
	ID	US-10-192-257-4	US-09-764-864-1205	US-10-021-811-16	US-10-021-811-4	US-10-021-811-14	US-09-956-993-2	US-09-956-993-4	US-09-838-561-8	US-09-816-760-8	US-09-757-049A-4	US-09-757-049A-5	US-09-757-049A-6	US-09-912-962-13	US-09-912-962-14	US-10-021-811-34	US-09-828-648-7	US-10-004-551-26	US-10-004-551-18	US-10-004-551-20
	DB	. 6	10	σ	6	6	σ	6	10	10	110	01	01	0	0.0	Ø	10	6	σ	თ
	Query Match Length DB	16	182	62	179	221	317	369	369	369	20	50	20	52	52	206	66	261	525	525
æ	Query Match	90.06	75.5	71.7	71.7	71.7	71.7	71.7	71.7	71.7	8.69	8.69	8.69	8.69	8.69	8.69	67.9	67.9	67.9	67.9
	Score	48	40	38	38	38	38	38	38	38	37	37	37	37	37	37	36	36	36	36
	Result No.	1	2	3	4	S	9	7	ω	σ	10	11	12	13	14	15	16	17	18	19

7.44	Sequence 22, Appl Sequence 23, Appl Sequence 76, Appl Sequence 96, Appl
9 US-10-004-551-22 9 US-11-004-551-24 9 US-11-004-551-14 9 US-10-004-551-16 9 US-00-909-667B-47 10 US-09-864-17-725 9 US-11-008-11BA-36 10 US-09-443-104-36 9 US-11-021-811-24 10 US-09-764-864-1171 9 US-10-021-811-62 10 US-09-764-864-1171 9 US-10-081-11BA-16 10 US-09-443-704-16 9 US-10-081-11BA-16 10 US-90-443-704-16 9 US-10-01-811-24 10 US-90-443-704-18 9 US-10-021-811-24 9 US-10-021-811-24 10 US-99-443-704-18 9 US-10-021-811-54 9 US-10-021-811-54 9 US-09-931-087A-1	10 US-09-931-087A-22 10 US-09-931-087A-23 9 US-10-021-811-28 10 US-09-751-100B-76 10 US-09-751-100B-96
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	576 576 103 109
	66.0 64.2 64.2 64.2
	3333 344 444
01000000000000000000000000000000000000	444 444 5

## ALIGNMENTS

RESULT 1

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Sequence 4, Application US/10192257
Publication No. US20030021786A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Liver, Lung and Esophagus
FILE REFERENCE: 1102665-0057
CURRENT APPLICATION NUMBER: US/10/192,257
CURRENT FILING DATE: 2002-07-09
PRIOR FILING DATE: 2001-07-09
PRIOR FILING DATE: 2001-07-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                                                    ; DB 9; Leuy...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1205, Application US/09764864;
Patent No. US20020132753A1;
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies;
FILE REFERENCE: PTZ23
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 48; DB 9; Pred. No. 0.03
                                                                                                                                                                                                                                                                                                                                                                         ; LOCATION: (1)...(1)
; OTHER INFORMATION: Xaa-pyroglutamic acid
US-10-192-257-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 90.6%; Sc
Best Local Similarity 100.0%; P
Matches 8; Conservative 0;
                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIn version 3.1
SEQ ID NO 4
LENGTH: 16
                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: MISC_FEATURE
                                                                                                                                                                                                                                                                                                                    ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 GPWLEEEE 9
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US-09-764-864-1205
US-10-192-257-4
                                                                                                                                                                                                                                                                                                      TYPE: PRT
                                                                                                                                                                                                                                                                                                                                           FEATURE:
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RESULT 5
US-10-021-811-14
Sequence 14, Application US/10021811
Sequence 14. Application US/10021811
Sequence 14. Application US/10021811
Sequence 14. Application US/0024007A1
GENERAL INFORMATION:
APPLICANT: Canon, Rebecca E.
APPLICANT: Gang, Yimen
APPLICANT: Wengy, Zude
TITLE OF INVENTION: Plant Myb Transcription Factor Homologs
FILE REFERENCE: B81294 US NA
CURRENT APPLICATION NUMBER: 0201-12-14
PRIOR APPLICATION NUMBER: 60/110,609
PRIOR APPLICATION NUMBER: 60/110,609
PRIOR FILING DATE: 1998-December-02
  Sequence 4, Application US/10021811
Publication No. US20030024007A1
GENERAL INFORMATION:
APPLICANT: Cahoon, Rebecca E.
APPLICANT: Cahoon, Rebecca E.
APPLICANT: Odell, Joan
APPLICANT: Weng, Zude
TITLE OF INVENTION: Plant Myb Transcription Factor Homologs
FILE REFERENCE: BB1294 US NA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 38; DB 9; Length 179;
Pred. No. 17;
3; Mismatches 1; Indels
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Pred. No. 21;
3; Mismatches
                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/10/021,811
CURRENT FILING DATE: 2001-12-14
PRIOR APPLICATION NUMBER: 60/110,609
PRIOR FILING DATE: 1998-December-02
NUMBER OF SEQ ID NOS: 63
SOFTWARE: Microsoft Office 97
LENGTH: 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Sequence 2, Application US/09956993; Patent No. US20020164733A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     71.78;
55.68;
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55.68;
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SOFTWARE: Microsoft Office 97
SEQ ID NO 14
LENGTH: 221
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Best Local Similarity 55.6
Matches 5; Conservative
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; ORGANISM: Oryza sativa
US-10-021-811-14
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Zea mays
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10 KGPWTEQED 18
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3 KGPWTEQED 11
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LOCATION: (177)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids US-09-764-864-1205
                                                                                                                                                                                                                                           LOCATION: (23)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                                                                                                                                                                                                                                                                                      LOCATION: (108)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                                                                                                                                                                                                                                                                                                                                                      LOCATION: (129)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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Sequence 16, Application US/10021811

Publication No. US20030024007A1

FUBLICATION NO. US20030024007A1

GENERAL INRORMATION:

APPLICANT: Cahoon, Rebecca E.

APPLICANT: Fang, Yiwen

APPLICANT: Fang, Yiwen

APPLICANT: Weng, Zude

TITLE OF INVENTION: Plant Myb Transcription Factor Homologs

FILE REFERENCE: BEL294 US NA

CURRENT APPLICATION NUMBER: US/10/021,811

CURRENT PILING DATE: 1998-December-02

FRIOR FILING DATE: 1998-December-02

NUMBER OF SEQ ID NOS: 63

SOFTWARE: Microsoft Office 97

SEQ ID NO 16

LENGTH: 62

TUBENGTH: 62
CURRENT APPLICATION NUMBER: US/09/764,864
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 1792
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1205
LENGTH: 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 40; DB 10; Length 182;
Pred. No. 8.2;
1; Mismatches 0; Indels
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Pred. No. 6;
3; Mismatches 1; Indels
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85.7%;
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Best Local Similarity 85.7
Matches 6; Conservative
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Best Local Similarity 55.6
Matches 5; Conservative
                                                                                                                                                     TYPE: PRT
ORGANISM: Homo sapiens
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10 KGPWTEQED 18
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164 PWMEEEE 170
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; LOCATION: (59)
US-10-021-811-16
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US-10-021-811-4
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Gaps

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A PAPLICANT: WEIL.

ITILE OF INVENTION:

TITLE OF INVENTION: MOLECULES ENCODING HUMAN ENZYME, AND USES THEREOF

TITLE OF INVENTION: MOLECULES ENCODING HUMAN ENZYME, AND USES THEREOF

FILE REFERENCE: CLOOLISHIDIV

CURRENT APPLICATION NUMBER: US/09/956,993

CURRENT FILING DATE: 2001-09-21
                                                             Gaps
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Length 221;
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; ORGANISM: Homo sapiens US-09-757-049A-4
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47 GPWLEE 52
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US-09-757-049A-4
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US-09-816-760-8
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LENGTH: 369
   LENGTH: 369
                                                         US-09-838-561-8
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                                                                                                                                                                                                                                                                                                                                                                         Sequence 4, Application US/09956993

Patent No. US20020164733A1

GENERAL INFORMATION:
APPLICANT: WEI, MIGHUI et al

TITLE OF INVENTION: ISOLATED HUMAN ENZYME, NUCLEIC ACID

TITLE OF INVENTION: MOLECULES ENCODING HUMAN ENZYME, AND USES THEREOF
FILE REPERENCE: CLOUISBLING US/09/956,993
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PRIOR APPLICATION NUMBER: 09/816,088
PRIOR FILING DATE: 2001-03-26
NUMBER OF SEQ ID NOS: 4
SEQ ID NO 2
LENGTH: 317
                                                                                                                                                                                 Score 38;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT FILLING DATE: 2001-09-21
PRIOR APPLICATION NUMBER: 09/816,088
PRIOR FILLING DATE: 2001-03-26
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4
LENGTH: 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Meyers, Rachel
APPLICANT: Cook, William James
APPLICANT: Williamson, Mark
APPLICANT: Wildiph-Owen, Laura A.
APPLICANT: Gimeno, Ruth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 8, Application US/09838561 Patent No. US20020042371A1
                                                                                                                                                                               71.78; $
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100.0%;
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Best Local Similarity 100.
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US-09-956-993-2
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Best Local Similarity
Matches 6; Conserv
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47 GPWLEE 52
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APPLICANT: BERNSTEIN, Harold S.

APPLICANT: BERNSTEIN, Harold S.

APPLICANT: COUGHLIN, Shaun R.

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR REGULATING CELL CYCLE

TITLE OF INVENTION: PROGRESSION

FILE REPERENCE: UCSP-020/020S

CURRENT APPLICATION NUMBER: US/09/757,049A

CURRENT FILING DATE: 1908-09-108

PRIOR PILING DATE: 1998-09-108

PRIOR APPLICATION NUMBER: US 60/060,688
                                                                                                                  Gaps
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                                                                  DB 10; Length 369; 34;
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Pred. No. 34;
0; Mismatches 0; Indels
                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Rudolph-owen, Laura A. 17TLE OF INVENTION: 22142, 21481, 25964, 21686, N. TITLE OF INVENTION: MOLECULES AND USES THEREFOR FILE REFERENCE: MNI-134CP
                                                    71.7%; Scor.
100.0%; Pred. No. 54,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/816,760 CURRENT FILING DATE: 2001-03-23 PRIOR APPLICATION NUMBER: 09/634,955 PRIOR FILING DATE: 2000-08-08 PRIOR FILING DATE: 2000-03-24 PRIOR FILING DATE: 2000-03-24 SUMBER OF SEQ ID NOS: 13 SOFTWARE: PATENTUM NUMBER OF SEQ ID NOS: 13
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100.08; Pre
0; !
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; Patent No. US20020127702A1
                                                                                                                                                                                                                                                                                                                    Sequence 8, Application US/09816760
Patent No. US2002005032A1
GENERAL INFORMATION:
APPLICANT: Mayers, Rachel
                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Cook, William James APPLICANT: Williamson, Mark
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 50
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 4
LENGTH: 50
                                                                Query Match 71.7
Best Local Similarity 100.
Matches 6; Conservative
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Best Local Similarity 100.
Matches 6; Conservative
ORGANISM: Homo sapiens
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Fatent No. US20020127702A1
GENERAL INFORMATION:
APPLICANT: BERNSTEIN, Harold S.
APPLICANT: COUGHLIN, Shaun R.
TITLE OF INVENTION: PROGRESSION
FILE REFERENCE: UCSF-020/020S
CURRENT APPLICATION NUMBER: US/09/757,049A
CURRENT FILING DATE: 1998-09-18
PRIOR FILING DATE: 1998-09-18
PRIOR FILING DATE: 1998-09-18
PRIOR FILING DATE: 1999-09-22
NUMBER OF SEQ ID NOS: 50
SOFTWARE: PatentIN Ver. 2/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 6, Application US/09757049A
Patent No. US20020127702A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: BERNSTEIN, Harold S.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR REGULATING CELL CYCLE
TITLE OF INVENTION: MPROGRESSION
FILE REFERENCE: UCSF-020/02US
CURRENT APPLICATION NUMBER: US/09/757,049A
CURRENT PILING DATE: 1090-01-01-08
PRIOR FILING DATE: 1998-09-18
PRIOR FILING DATE: 1998-09-18
PRIOR FILING DATE: 1998-09-22
NUMBER OF SEQ ID NOS: 50
SOFTWARE: PATENTIN VOINS: 2.1
SEQ ID NO 6
LENGTH: 50
                                     Gaps
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Score 37; DB 10; Length 50;
Pred. No. 7;
                                     1; Indels
                                    3; Mismatches
69.8%;
55.6%;
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55.6%;
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55.6%;
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Best Local Similarity 55.6
Matches 5; Conservative
                                    5; Conservative
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Best Local Similarity 55.6
Matches 5; Conservative
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                  Best Local Similarity
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2 KGPWTKEED 10
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2 KGPWTKEED 10
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2 KGPWTKEED 10
                                                                        1 EGPWLEEEE 9
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US-09-757-049A-6
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                                                                                                                                                                 RESULT 11
US-09-757-049A-5
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 Query Match
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                                  Matches
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TITLE OF INVENTION: TELOMERE REPEAT BINDING FACTOR AND
DIAGNOSTIC AND THERAPEUTIC USE THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ó
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TITLE OF INVENTION: TELOMERE REPEAT BINDING FACTOR AND
DIAGNOSTIC AND THERAPEUTIC USE THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   69.8%; Score 37; DB 10; Length 52; 55.6%; Pred. No. 7.3; 1: Indels 1:ve 3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/018,635
FILING DATE: 04-FEB-1998
ATTORNEY/AGENT INFORMATION:
NAME: David A. Jackson
REGISTRATON NUMBER: 26,742
REFERRNCE/POCKET NUMBER: 600-1-142 CIP1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/09/912,962
FILING DATE: 25-Jul-2001
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-09-912-962-13
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CORRESPONDENCE ADDRESS: ADDRESSEE: KLAUBER & JACKSON
STREET: 411 Hackensack Avenue
                                                                                                                                                                                                                                                                                            STREET: 411 Hackensack Avenue
                                                                                                             APPLICANT: de Lange, Titia
Broccoli, Dominique
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Broccoli, Dominique
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 14, Application US/09912962 Patent No. US20020076719A1 GENERAL INFORMATION:
                                          Sequence 13, Application US/09912962
Patent No. US20020076719A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 52 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: de Lange, Titia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 13:
                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: KLAUBER
                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 52
                                                                                                                                                                                                                                                                                                                                         STATE: New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
                                                                                                                                                                                                                                                                                                                      CITY: Hackensack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 07601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
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3 KGPWTKEED 11
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RESULT 13
US-09-912-962-13
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US-09-912-962-14
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Sequence 34, Application US/10021811

Publication No. US2030024007A1

GENERAL INFORMATION:

APPLICANT: Canbon, Rebecca E.

APPLICANT: Gandon, Nawen

APPLICANT: Odell, Joan

APPLICANT: OF INVENTION: Plant Myb Transcription Factor Homologs

FILE PEFERRNCE: Bal294 US NA

CURRENT APPLICATION NUMBER: US/10/021,811

CURRENT FILING DATE: 1998-December-02

NUMBER OF SEQ ID NOS: 63

SOFTWARE: Microsoft Office 97

SEQ ID NO 34

LENTH: 206

MUNDEL 1000
                                                                                                                      MEDION TIEM FOR COMPATIBLE
COMPUTER: IEM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/912,962
FILING DATE: 25-Jul-2001
CLASSIFICATION NUMBER: 09/018,635
APPLICATION NUMBER: 09/018,635
FILING DATE: 04-FEB-1998
ATTORNEY/AGENT INFORMATION:
NAME: DAYLO A-FEB-1998
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 26,742
TELERAX: 201-343-1684
TELERAX: 201-343-1684
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARAPENSTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             69.8%; Score 37; DB 9; Length 206; 55.6%; Pred. No. 28; 1: Indels 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 69.8%; Score 37; DB 10; Length 52; Best Local Similarity 55.6%; Pred. No. 7.3; Matches 5; Conservative 3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDRESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-09-912-962-14
                                                                                                            MEDIUM TYPE: Floppy disk
                                                            ZIP: 07601
COMPUTER READABLE FORM:
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 55.6
Matches 5; Conservative
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; ORGANISM: Glycine max
US-10-021-811-34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             :||| :||:
3 KGPWTKEED 11
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16 KGPWIMEED 24
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US-10-021-811-34
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Search completed: February 5, 2003, 09:56:01 Job time : 6.85714 secs

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GenCore version 5.1.3 Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

February 5, 2003, 09:46:31; Search time 11.5714 Seconds (without alignments) US-09-700-329-1 53 1 EGPWLEEEE 9 Scoring table: Perfect score: Sednence: Run on: Title:

BLOSUM62 Gapop 10.0 , Gapext 0.5

283224 Total number of hits satisfying chosen parameters:

283224 seqs, 96134422 residues

Searched:

length: 0 length: 2000000000 Minimum DB seq Maximum DB seq

Post-processing: Minimum Match 1008
Maximum Match 1008
Listing first 45 summaries

pir1:\*
pir2:\*
pir3:\* PIR\_73:\*

Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	biq qastrin - Nort	rin precur			gastrin precursor			¥	qastrin precursor			deoxyhypusine synt		Ω.		Ω	myb-related protei	big gastrin [valid		ŭ		probable MYB trans	class I major hist	las	ajo	I major	I major		Q
SUMMARIES	QI	A60506	GMHUB	GMCT	A60071	GMPGB	GMDG	GMSH	JS0426	GMBO	T46166	A29541	C75119	F64401	C91080	D85925	JQ2390	T09758	GMGPB .	B29541	S20350	JQ0961	A71448	C35878	A49885	E35878	A35878	B35878	S11246	T00808
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	Query	94.3	94.3	94.3		90.6	9.06	88.7	88.7	88.7	84.9	81.1	81.1	79.2	7.4	7.4	7.4	7.4	5.5	5.5	5.5	•		٠		•	•	3.6	3.6	3.6
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	Score	50	20	50	48	48	48	47	47	47	45	43	43	42	41	41	41	41	40	40	40	40	40	39	39	39	39	39	39	39
	Result No.	7		e	4	Ŋ	9	7	8	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29

	myb-related transc	Myb DNA binding pr	myb-related protei	probable transcrip	N-acetylqlucosamin	myb-like protein -	hypothetical prote	alpha-actinin - Ca	hypothetical prote	hypothetical prote	probable tenascin	napin nIb - rape	MJ0653 homolog AF0	conserved hypothet	SEC14 protein - ve	R2R3-MYB transcrip
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<b>-</b> -1	•															
	T51666	T49254	T03850	T51509	D82158	T48253	T26149	A48403	T26147	T41135	T09070	S26636	669355	F69335	A37766	T45859
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	71.7	71.7	71.7	71.7	71.7	71.7	71.7	71.7	71.7	71.7	71.7	8.69	8.69	8.69	8.69	8.69
	38	38	38	38	38	38	38	38	38	38	38	37	37	37	37	37
	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

RESULT 1
A60506
big gastrin - North American opossum
N;Contains: gastrin
C;Species: Didelphis virginiana, Didelphis marsupialis virginiana (North American opocybate: 19-Mar-1993 #sequence\_revision 19-Mar-1993 #text\_change ll-May-2000
C;Accession: A60506
R;Shinomura, Y.; Eng, J.; Rattan, S.C.; Yalow, R.S.
Comp. Biochem. Physiol. B 96, 239-242, 1990
A;Title: Opossum (Didelphis virginiana) "little" and "big" gastrins.
A;Reference number: A60506; MUID:90298616; PMID:2361360
A;Residues: 1-33 <SHI>
C;Superfamilly: gastrin
B;Superfamilly: gastrin #status experimental <AMATD>
E;18-33/Product: gastrin #status experimental <AMATD>
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;28/Binding site: sulfate (Tyr) (covalent) (partial) #status experimental
F;38/Binding site: amidated carboxyl end (Phe) #status experimental

Query Match

Gaps . 0 Score 50; DB 2; Length 33; Pred. No. 0.037; 1; Mismatches 0; Indels 94.38; 88.98; Best Local Similarity 88.9 Matches 8; Conservative

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RESULT 2

Gartin precursor [validated] - human
N;Contains: big gastrin; cryptagastrin; gastrin-17
C;Species: Homo sapiens (man)
C;Specie

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Nicontains: big gastrin (gastrin 34); gastrin (contains) big gastrin (gastrin 34); gastrin (contains) big gastrin (gastrin 34); gastrin (contains) big gastrin (contains) big salvestris catus (domestic cat) (c) bate: 13-Jun-1983 #sequence_revision 02-Jun-1994 #text_change 20-Oct-2000 (c) bate: 13-Jun-1983 #sequence_revision 02-Jun-1994 #text_change 20-Oct-2000 (c) big salvestrin (c) big salv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Molecule type: protein A;Residues: 76-92 <REW> A;Residues: 36-92 <REW> A;Note: gastrin-6 isolated from gastric mucosa and blood is fully active; sulfation o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C.Superfamily: gastrin

C.Superfamily: gastrin

C.Superfamily: gastrin

C.Steywords: amidated carboxyl end; phosphoprotein; pyroglutamic acid; sulfoprotein

C.Steywords: amidated carboxyl end; properties (SIG)

F) 1-21/Domain: signal sequence #status predicted (SIG)

F; 2-56/Product: cryptagastrin #status experimental CAGNN>

F; 7-92/Product: gastrin #status experimental CAGN>

F; 5-92/Product: gastrin-f #status experimental CAGN>

F; 5-92/Product: gastrin-f #status experimental CAGNS>

F; 5-92/Product: gastrin-f #status experimental CAGNS>

F; 597/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #link BGN #sta

F; 7/Runding site: sulfate (Tyr) (covalent) (partial) #status experimental

F; 92/Modified site: amidated carboxyl end (Phe) (amide in mature form from following
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: mRNA
A; Residues: 1-104 <KIMS
A; Cross-references: EMBL:X16582; NID:g1099; PIDN:CAA34599.1; PID:g1100
A; Cross-references: EMBL:X16582; NID:g1099; PIDN:CAA34599.1; PID:g1100
B; Agarwal, K.L.; Kenner, G.W.; Sheppard, R.C.
J. Am. Chem. Soc. 91, 3096-3097, 1969
A; Title: Feline gastrin. An example of peptide sequence analysis by mass spectrometry
                                                                                                                                                                A.Cross-references: EMBL:V00511; NID:g31654; PIDN:CAA23769.1; PID:g31655
R;Rehfeld, J.F.; Johnsen, A.H.
Eur. J. Bloochen. 233, 765-773; 1994
A;Title: Identification of gastrin component I as gastrin-71. The largest possible A;Reference number: $48183; MUID:94333379; PMID:8055952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A.Residues: 1-101 <KAR>
A.Cross-references: GB:M15958; NID:9182990; PIDN:AAA52520.1; PID:9182991
R.Rehfeld, J.F.; Hansen, C.P.; Johnsen, A.H.
EMBO J. 14, 389-396, 1995
A.Fitle: Post-poly(Glu) cleavage and degradation modified by O-sulfated tyrosine: 6787eference number: S54350; MUID:95137019; PMID:7530658
A.Reference number: S54350; MUID:95137019; PMID:7530658
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A.Status: preliminary
A.Molcoule type: procein
A.Residues: 22-40 (REM>
R:Kariya, Y.; Kato, K.; Hayashizaki, Y.; Himeno, S.; Tarui, S.; Matsubara,
Gene 50, 345-352, 1986
A:Title: Expression of human gastrin gene in normal and gastrinoma tissues.
A.Reference number: 154006; MUID:87219893; PMID:3034736
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88.9%; Pred. No. 0.13;
Live 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Gene: GDB:GAS
A;Cross-references: GDB:119261; OMIM:137250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Status: translated from GB/EMBL/DDBJ
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Best Local Similarity
Matches 8; Conserv
                                                                A; Molecule type: mRNA
A; Residues: 1-101 <RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Map position: 17q-17q
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                         A/Cross-references: 08:X00183, NID:931648; PIDN:CAA25005.1; PID:931649
R/HATIS, J. L. I. Kenner, E. W.

unpublished results, cited by Gregory, R.A., and Tracy, H.J., in Gastrointestinal Hormon
A/Reference number: A94473
A/Rolecule rype: protein
A/Rosidues: 59-64.7 H./66, S/68-92 capr.
A/Rosidues: A/Romer, G.W.: Sheppard, R.C.
A/Rote on mumber: A/Romer, G.W.: Sheppard, R.C.
A/Rosidues: A/Romer, G.W.: Sheppard, R.C.
A/Rosidues: A/Romer, G.W.: Sheppard, R.C.
A/Rote on mumber: A/Romer, G.W.: Sheppard, A/Romer, G.W.: Sheppard, A/Romer, G.W.: A/Romer, G.W.: Sheppard, A/Romer, A/Romer, G.W.: A/Romer, G.W.: Sheppard, A/Romer, G.W.: A/Romer, A/Romer, G.W.: A/Romer, A/Romer, G.W.: A/Romer, A/Romer, G.W.: A/Romer, G.W.: A/Romer, G.W.: A/Romer, G.W.: A/Romer, G.W.: A/Romer, 
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A; Molecule type: protein
A; Residues: 22-51 cHUED:
B; R; Higashimoto, Y.; Himeno, S.; Shinomura, Y.; Nagao, K.; Tamura, T.; Tarui, S.
Biochem. Biophys. Res. Commun. 160, 1364-1370, 1989
A; Title: Purlification and structural determination of urinary NH-2-terminal big gastrin A; Reference number: A32487; MUID:89273602; PMID:2730647
A; Accession: A32487
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R;Boel, E.; Vuust, J.; Norris, F.; Norris, K.; Wind, A.; Rehfeld, J.F.; Marcker, K.A.
Proc. Natl. Acad. Sci. U.S.A. 80, 2866-2869, 1983
A;Title: Molecular cloning of human gastrin cDNA: evidence for evolution of gastrin by
A;Reference number: I37408; MUID:83221503; PMID:6574456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A Residues: 59-66 Aliable
A Residues: 59-68 Aliable
A Residues: 59-69 A Residues: 59-69 A Residues: 59-69 A Residues: 59-69 A Residues: 59-64 
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A; Residues: 59-67 <H12>
A; Experimental source: urine
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A; Residues: 1-101 <KAT>
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A.Status: preliminary
A.Molecule type: protein
A.Rosidues: 97-104 CDES
A.Residues: 97-104 CDES
C.Superfamily: gastrin
C.Reywords: amidated carboxyl end; phosphoprotein; pyroglutamic acid; sulfoprotein
C.Reywords: amino terminal propeptide #status predicted <PRO>
F:1-21/Domain: amino terminal propeptide #status predicted <PRO>
F:59-92/Product: big gastrin #status experimental <PGN>
F:59-92/Product: gastrin #status experimental <PGN>
F:59-92/Product: gastrin #status experimental <PGN>
F:59/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status experimental F;92/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status experimental F;92/Modified site: amidated carboxyl end (Phe) (amide in mature form from following F;96/Binding site: phosphate (Ser) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: GB:M25036; NID:g164626; PIDN:AAA31111.1; PID:g164627
R;Desmond, H.; Varro, A.; Young, J.; Gregory, H.; Nemeth, J.; Dockray, G.J.
Regul, Pept. 25, 223-233, 1989
A;Title: The constitution and properties of phosphorylated and unphosphorylated C-ter A;Reference number: A60070; MUID:89331947; PMID:2756156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          M.A.; Gregory, R.A.; Hardy, P.M.; Kenner, G.W.; MacLeod,
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N; Contains: big gastrin; gastrin

G; Species: Canis Lupus familiaris (dog)

C; Decies: Canis Lupus familiaris (dog)

C; Accession: B61053; A61053; JS0425; A01620; B60070

C; Accession: B61053; A61053; JS0425; A01620; B60070

C; Accession: B61053; A61053; JS0425; A01620; B60070

A; Right: Cioning of canine gastrin cDNA's encoding variant amino acid sequences. A; Reference number: A61053; MUD:91085716; PMID:2262079

A; Accession: B61053

A; Accession: B61053

A; Residue: not compared with conceptual translation

A; Molecule type: mRNA

A; Residues: 1-104 < GAN>

A; Residues: 1-104 < GAN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    using an oligonucleotide probe. PMID: 6930858
                                 A; Accession: 1994473
A; Molecule type: protein
A; Residues: 59-64, THPP, 168-92 < HAR>
A; Nesidues: 59-64, THPP, 168-92 < HAR>
A; Note: Tyr-87 is sulfated in two-thirds of the molecules
A; Note: this peptide was extracted from the antral mucosa
B; Gregory, H.; Hardy, P. M.; Jones, D.S.; Kenner, G.W.; Sheppard,
Nature 204, 931-933, 1964
A; Title: The antral hormone qastrin.
A; Reference number: A93148
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Contents: annotation; synthesis
R; Agarwal, K.L; Noyes, B.E.
Ann. N. Y. Acad. Sci. 343, 433-442, 1980
A; Title: Studies on gastrin mRNA structure
A; Reference number: 146622; MUID:80240380;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Accession: I46622
A;Status: translated from GB/EMBL/DDBJ
KMolecule type: mRNA
A;Residues: 56-82 <AGA>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R; Anderson, J.C.; Barton,
Nature 204, 933-934, 1964
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A; Molecule type: protein
A; Residues: 76-92 <GRE>
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A; Residues: 1-104 < YOO>
A; Residues: 1-104 < YOO>
A; Cross-references: CSV01303; GB:J00651; NID:g1846; PIDN:CAA24610.1; PID:g1847
B; Harris, J.1.; Kenner, E.W.
unpublished results, cited by Gregory, R.A., and Tracy, H.J., in Gastrointestinal Hormon
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R.Yu, J.; Xin, Y.; Eng, J.; Yalow R.S.

A.Title: Rhesus monkey gastroenteropancreatic hormones: relationship to human sequences. A. Reference number: A60071; MUID:91164506; PMID:2003150

A. Accession: A60071

A. Accession: A60071

A. Molocule type: protein

A. Residues: 1-17 < VUA>
C. Superfamily: gastrin

A. Residues: 1-17 < VUA>
C. Superfamily: gastrin

F. L. Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F: 12/Binding site: sulfate (Tyr) (covalent) (partial) #status experimental

F: 17/Modified site: amidated carboxyl end (Phe) #status experimental
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A. Accession: A61074
A. Molecule type: protein
C. Superfamily: gastrin
C. Superfamily: gastrin
F. 1-19/Domain: signal sequence #status predicted ASIG>
F. 59-92/Product: big gastrin #status experimental AMAT>
F. 76-92/Product: dastrin #status experimental AMAT>
F. 76-92/Product: gastrin #status experimental AMAT>
F. 76-92/Product: 
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gastrin precursor [validated] - pig
C:Species: Sus scrofa domestica (domestic pig)
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 17-Dec-1982 #sequence_revision 17-Dec-1982 #text_change 31-Dec-2000
C:Accession: A93903; B94473; A93148; I46622; A60070; A01618
R:Yoo, O.J.; Powell, C.T.; Agarwal, K.L.
Proc. Natl. Acad. Sci. U.S.A. 79, 1049-1053, 1982
A;Title: Molecular cloning and nucleotide sequence of full-length cDNA coding for paracesion: A93903; MUID:82174533; PMID:6951161
A;Accession: A93903
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C;Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 20-Mar-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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Pred. No. 0.14;
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                                                                                       A;Molecule type: protein
A;Mesidues: 76-92 <AGA>
R;Eng, J.; Du, B.H.; Johnson, G.F.; Kanakamedala, S.; Samuel,
Regul. Pept. 37, 9-13, 1992
A;Title: Cat gastrinoma and the sequence of cat gastrins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                     A, Title: Cat gastrinoma and the sequende of cat gastrins.
A, Reference number: A61074; MUID:92262853; PMID:1585019
A; Reference number: A01621; MUID:69206035; PMID:5784957
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Pred. No. 0.039;
2; Mismatches
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88.9%;
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Best Local Similarity 88.9
Matches 8; Conservative
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nes 7; Conserv
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Matches
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Gaps

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R;Bonato, C.; Eng, J.; Hulmes, J.D.; Miedel, M.; Pan, Y.C.E.; Yalow, R.S. Peptides 7, 689-693, 1986
A;Title: Sequences of gastrins purified from a single antrum of dog and of goat. A;Reference number: JS0425; MUID:87016557; PMID:3763441
                                                                                              big gastrin - goat
N;Contains: gastrin
C;Species: Capra aegagrus hircus (domestic goat)
C;Date: 30-Sep.1993 #sequence_revision 30-Sep-1993 #text_change 20-Mar-1998
C;Accession: JS0426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                88.7%;
77.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 7; Conserv
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A;Introns: 71/1
                                         RESULT 8
JS0426
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C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Date: 13-Jun-1983 #sequence_revision 13-Jun-1983 #text_change 20-Mar-1998
C;Date: 13-Jun-1983 #sequence_revision 13-Jun-1983 #text_change 20-Mar-1998
C;Accession: A01619, Bentley, P.H.; Gregory, R.A.; Kenner, G.W.; Sheppard, R.C. Nature 219, 614-615, 1968
Nature 219, 614-615, 1968
A;Title: Isolation, structure and synthesis of ovine and bovine gastrins.
A;Reference number: A01619; MUID:68357500; PMID:5665711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C; Superfamily: gastrin
C; Superfamily: gastrin
C; Keywords: amidated carboxyl end; hormone; pancreas; phosphoprotein; pyroglutamic acid;
F; 1-21/Domain: signal sequence #status experimental <MGP>
F; 59-92/Product: big gastrin #status experimental <MGAP>
F; 76-92/Product: gastrin #status experimental 
F; 76-92/Product: gastrin #status experimental F; 97-Modified site: sulfate (Tyr) (covalent) (partial) #status experimental F; 96/Binding site: midated carboxyl end (Phe) (amide in mature form from following gly F; 96/Binding site: phosphate (Seq) (covalent) (partial) #status experimental
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C:Keywords: amidated carboxyl end; hormone; pancreas; phosphoprotein; pyroglutamic acid;
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F:12/Binding site: sulfate (Tyr) (covalent) / partial) #status experimental
F:17/Modified site: amidated carboxyl end (Phe) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: protein
A; Residues: 76-82, 'A', 84, 'E', 86-92 < AGA>
R; Residues: 76-82, 'A', 84, 'E', 86-92 < AGA>
R; Desmond, H.; Varro, A.; Young, J.; Gregory, H.; Nemeth, J.; Dockray, G.J.
R; Desmond, H.; Varro, A.; 1989
A; Title: The constitution and properties of phosphorylated and unphosphorylated C-termin
A; Reference number: A60070; MUID; 89331947; PMID: 2756156
A; Accession: B60070
A;Residues: 1-84,'T',86-104 <GA2>
A;Note: it is unclear whether the sequence difference results from polymorphism, multipl
R;Bonato, C.; Eng, J.; Hulmes, J.D.; Miedel, M.; Pan, Y.C.E.; Yalow, R.S.
Peptides 7, 689-693, 1986
                                                                                                                              goat.
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                                                                                                                   A;Title: Sequences of gastrins purified from a single antrum of dog and of A;Reference number: JS0425; MUID:87016557; PMID:3763441 A;Accession: JS0425
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C; Comment: Big gastrin constitutes only about 5% of antral gastrin.
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                                                                                                                                                                                                                                                                A; Experimental source: antral mucosa
A; Note: about 10% of gastrin is sulfated
R; Agarwal, K.L.; Kenner, G.W.; Sheppard, R.C.
Experientia 25, 346-348, 1969
A;Title: Structure and synthesis of canine gastrin.
A;Reference number: A01620; MUID:69253357; PMID:5799207
A;Accession: A01620
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Pred. No. 0.057;
2; Mismatches
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ilarity 77.8%;
Conservative 2
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Best Local Similarity
7; Conserv?
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A, Residues: 1-17 <AGA>
C, Superfamily: gastrin
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A; Residues: 59-92 <BON>
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Best Local Similarity
Matches 7; Conserv
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1 QGPWVEEEE 9
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Gaps

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Length 34; 0; Indels

Score 47; DB 2; Pred. No. 0.12; Mismatches

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C;Superfamily: gastrin
C;Keywords: amidated carboxyl end; hormone; pancreas; phosphoprotein; pyroglutamic ac
F;1-19/Domain: signal sequence *status predicted <SIG>
F;59-92/Product: big gastrin *status predicted <GGN>
F;76-92/Product: gastrin *status experimental <SGN>
F;76-92/Product: gastrin *status experimental <SGN>
F;76-92/Product: gastrin *status experimental <SGN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A.Molecule type: mRNA
A.Residues: 1-104 <KIM>
A.Residues: 1-104 <KIM>
A.Residues: 1-104 <KIM>
A.Residues: 1-104 <KIM>
B.Lund, T.; Olsen, J.; Rehfeld, J.F.

Mol. Endocrinol. 3, 1565-1588, 1989
A.Title: Cloning and Sequencing of the bovine gastrin gene.
A.Title: Cloning and Sequencing of the bovine gastrin gene.
A.Reference number: A41409; MUID:90114160; PMID:2608050
A.Recession: A41409
A.Residues: 1-31, L', 33-36, R', 38-47, T', 49-73, 'N', 75-80, 'G', 82-95, 'M', 97-98, 'G', 100-A; Residues: 1-31, L', 33-36, 'R', 38-47, 'T', 49-73, 'N', 75-80, 'G', 82-95, 'M', 97-98, 'G', 100-A; Cross-references: GB:M3167; NID:9163079; PIDN:AAA30537.1; PID:9163080
A.Residues: the authors translated the codon CTG for residue 32 as Ala, AAT for residue 3 A,NOLE: Lassidue 32 as Ala, AAT for residue 3 R, Agarwal, K.L.; Beacham, J.; Bentley, P.H.; Gregory, R.A.; Kenner, G.W.; Sheppard, Rature 219, 614-615, 1968
                                                        C; Species: Bos primigenius taurus (cattle)
C; Date: 31-Dec-1991 #sequence_revision 23-Mar-1995 #text_change 20-Oct-2000
C; Date: 31-Dec-1991 #sequence_revision 23-Mar-1995 #text_change 20-Oct-2000
C; Accession: S14400; A41409; B01619; A01619
R; Kim, S.J.; Uhm, K.N.; Kang, Y.K.; Yoo, O.J.
BNA Seq. 1, 181-187, 1991
A; Title: Bovine and feline gastrin cDNA sequences and the amino acid and nucleotide s A; Reference number: S14400; MUID:92127058; PMID:1773057
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A,Title: Isolation, structure and synthesis of ovine and bovine gastrins A;Reference number: A01619; MUID:68357500; PMID:5665711
gastrin precursor [validated] - bovine
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Gaps

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Length 335; Indels

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C; Accession: C75119
R; anonymous, Genoscope
submitted to the EMBL Data Library, July 1999
A; Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome s
A; Reference number: A7501
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-335 < KAN>
A;
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A; Residues: 1-248 <HAY>
A; Cross-references: GB:BA000007; PIDN:BAB37034.1; PID:913363082; GSPDB:GN00154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 81.1%; Score 43; DB 2;
77.8%; Pred. No. 7.8;
iive 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         llarity 77.8%;
Conservative
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Matches 7; Conserv
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A; Residues: 1-370 <BUL>
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deoxyhypusine synthase (EC 2.5.1.46) dysl PAB0511 [similarity] - Pyrococcus abyssi (stra
C;Species: Pyrococcus abyssi
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Nov-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N:Alternate names: protein T402.130
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 04-Mar-2000
C;Accession: T46166
R;Nyakatura, G; Fartmann, B; Dauner, D; Sterr, W; Holland, R; Weichselgartner, M.; Submitted to the Protein Sequence Database, December 1999
A;Reference number: 223025
A;Accession: T46166
       F;76/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status experimen F;87/Binding site: sulfate (Tyr) (covalent) (partial) #status experimental F;92/Modified site: amidated carboxyl end (Phe) (amide in mature form from following gly
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A;Note: T4D2.130
C;Superfamily: Arabidopsis myb-related protein 2; myb DNA-binding repeat homology
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C;Species: Chinchilla brevicaudata, Chinchilla lanigera brevicaudata
C;Species: Chinchilla brevicaudata, Chinchilla lanigera brevicaudata
C;Sacession: A3541
R;Shinomura, Y.; Eng, J.; Yalow, R.S.
Biochem. Biophys. Res. Commun. 143, 7-14, 1987
A;Title: Chinchilla "big" and "little" gastrins.
A;Teterence number: A90130; MUID:87156784; PMID:3827930
A;Accession: A29541
A;Molecule type: protein
A;Residues: 1-16 <SHI>
C;Superfamily: gastrin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                           Score 47; DB 1; Length 104;
Pred. No. 0.44;
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0.25;
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87.5%; Pred. No.
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A;Molecule type: DNA
A;Residues: 1-238 <NYA>
A;Cross-references: EMBL:AL132958
A;Experimental source: cultivar
                                                                                                                                                   88.78;
                                                                                                                                                                               77.88;
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Matches 7; Conservative
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Matches 7; Conservative
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Best Local Similarity
Matches 7; Conserv
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76 QGPWVEEEE 84
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| EGPWAEEE 8
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decyyhypusine synthase (EC 2.5.1.46) MJ0814 [similarity] - Methanococcus jannaschii Gispecies: Methanococcus jannaschii C;Species: Mether, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blak ; Reiut, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blak ; Reinc, C.I.; White, P.W.; Mirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, Science 273, 1058-1073, 1996
A;Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese A;Authors: Raine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese A;Reference number: A64300; MUID:96337999; PMID:8688087
A;Accession: F64401
A;Stellminary; nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: GB:U67525; GB:L77117; NID:92826325; PIDN:AAB98813.1; PID:91591503
C;Genetics:
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C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001
C;Date: 18-Jul-2001
B;Hayashi, T.: Makino, K.: Ohnishi, M.: Kurokawa, K.: Ishii, K.: Yokoyama, K.: Han, Gasawara, N.: Yasunaga, T.: Kuhara, S.; Shiba, T.: Hattori, M.: Shinagawa, H.
DMA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and GA;Reference number: A99629; MUID:21156231; PMID:11258796
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hypothetical protein 24066 [imported] - Escherichia coli (strain O157:H7, substrain EDL9 C:Species: Escherichia coli (c) adeci Beb-2001 #text_change 14-Sep-2001 C:Species: Escherichia coli (c) adeci B6502 Bequence_revision 16-Feb-2001 #text_change 14-Sep-2001 C:Species: D:Species: D:Sp
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77.4%; Score 41; DB 2; Length 248; Best Local Similarity 66.7%; Pred. No. 12; Matches 6; Conservative 2; Mismatches 1; Indels
A;Experimental source: strain O157:H7, substrain RIMD 0509952 C;Genetics:
A;Gene: ECs3611
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234 QGPWLSKEE 242
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234 QGPWLSKEE 242
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58.067 Million cell updates/sec
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                                           2003, 09:41:15; Search time 6.42857 Seconds
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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                           112892 seqs, 41476328 residues
                                                                                                                                                                                                                                                        SUMMARIES
                                                                                                                                                                                                                                                                                           GAST_DIDMA
GAST_HUMAN
GAST_FELCA
GAST_MACMU
GAST_CANFA
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2SSI_BRANA
LAG3_HUMAN
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SC14_KLULA
ERA_CAUCR
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MYB_XENLA
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GAST_HORSE
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ZIM3_HUMAN
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MYB_BOVIN
MYB_HUMAN
                             - protein search, using sw model
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Maximum DB seq length: 2000000000
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Match Length
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gallus gall
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homo sapien
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"Opossum (Didelphis virginiana) 'little' and 'big' gastrins.";
"Opossum (Didelphis virginiana) 'little' and 'big' gastrins.";
-:- Comp. Biochem. Physiol. 968.239-242(1990).
-:- FUNCTION: Gastrin stimulates the stomach mucosa to produce and secrete hydrochloric acid and the pancreas to secrete its digestive enzymes. It also stimulates smooth muscle contraction and increases blood circulation and water secretion in the stoma
                                                                                                                                                                                                                                                                                                                                                                                                                      -1- SUBCELLULAR LOCATION: Secreted.
-1- SIMILARITY: BELONGS TO THE GASTRIN/CHOLECYSTOKININ FAMILY.
PIR; A60506, A60506.
InterPro; IPRO01651; Gastrin.
PROSITE; P600218; Gastrin; 1.
PROSITE; P600259; GASTRIN; 1.
HORNONE; Cleavage on pair of basic residues; Amidation; Sulfation.
PEPTIDE 18 33 GASTRIN (GASTRIN 33).
                                                                                                                                                                                                                                                                    Didelphis marsupialis virginiana (North American opossum).
Sukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia; Metatheria; Didelphimorphia; Didelphidae; Didelphis.
NCBL_TaxID=9267;
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                                                 P10243
P52550
P46036
O78422
P48313
Q9Y2h8
P10244
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217D28C15027B661 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 2
GAST_HUMAN STANDARD; PRT; 101 AA.
DG 0350; P78464; P78463;
DT 21-JUL-1986 (Rel. 01, Created)
DT 23-OCT-1986 (Rel. 02, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Gastrin precursor.
                                                                                                                                                                                                                            28, Last sequence update)
                                                                                                                                                                                                33 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. 0.02
L: Mismatches
                                                                                                                                           ALIGNMENTS
                                                                                        TERM_ADE40
Y972_HUMAN
Z33A_HUMAN
                                       MYBA_MOUSE
MYBA_HUMAN
MYBA_CHICK
FER3_PLEBO
YC65_GUITH
                    MYBA_XENLA
MYBB_XENLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SULFATION
           MYBB_MOUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score
                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                      SEQUENCE.
MEDLINE=90298616; PubMed=2361360;
                                                                                                                                                                                                                   Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               94.3%;
88.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3856 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8; Conservative
                                                                                                                                                                                               STANDARD;
700
704
728
743
751
751
757
757
96
                                                                                         646
683
810
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28
33
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28,
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Best Local Similarity
                                                                                                                                                                                                                           (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                 and intestine.
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18
18
28
33
AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            33
                                                                                                                                                                                                                           01-FEB-1994
15-JUN-2002
                                                                                                                                                                                                                                                Big gastrin.
GAS.
                                                                                                                                                                                            GAST_DIDMA P33713;
                                                                                                                                                                                                                 01-FEB-1994
 MOD_RES
MOD_RES
SEQUENCE
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PEPTIDE
MOD_RES
MOD_RES
                                                                                                                                                                                   GAST_DIDMA
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Matches
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                                                                     SEQUENCE FROM N.A.
MEDLINE-87219893; PubMed-3034736;
Kariya Y., Kato K., Hayashizaki Y., Himeno S., Tarui S., Matsubara K.;
Expression of human gastrin gene in normal and gastrinoma tissues.";
Gene 50:345-352(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-84144842; PubMed-6322186; Miborg O., Berglund L., Boel E., Norris F., Norris K., Rehfeld J.F., Marcker K.A., Vuust J.; Marcker K.A., Vuust J.; "Structure of a human gastrin gene."; Proc. Natl. Acad. Sci. U.S.A. 81:1067-1069(1984).
                                                                                                                                                                                                                                                                                                                                                       "Molecular cloning of human gastrin cDNA: evidence for evolution of gastrin by gene duplication.";
Proc. Natl. Acad. Sci. U.S.A. 80:2866-2869(1983).
                                                                                                                                                                      Ito R., Sato K., Helmer T., Jay G., Agarwal K.L.;
Structural analysis of the gene encoding human gastrin: the large
intron contains an Al. sequence ".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Purification and structural determination of urinary NH2-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=94333379; PubMed=8055952;
Rehfeld J.F., Johnsen A.H.;
Identification of gastrin component I as gastrin-71. The largest
possible bloactive progastrin product.";
Eur. J. Blochem. 223:765-773(1994).
                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE-84169471; Pubmed-6324077;
Kato K., Hayashizaki Y., Takahashi Y., Himeno S., Matsubara K.;
"Molecular cloning of the human gastrin gene.";
Nucleic Acids Res. 11:8197-8203(1983).
                                                                                                                                                                                                                                                                                             [4]
SEQUENCE FROM N.A.
MEDLINE-83221503; PubMed-6574456;
Boel E., Vuust J., Norris F., Norris K., Wind A., Rehfeld J.F.,
Marcker K.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-89273602; PubMed-2730647;
Higashimoto Y., Himeno S., Shinomura Y., Nagao K., Tamura T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-84159488; Pubmed-6689486;
Kato K., Himeno S., Takahashi Y., Wakabayashi T., Tarui
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-69298172; PubMed-5822140; Grossman M.I.; Gregory R.A., Tracy H.J., Agarwal K.L., Grossman M.I.; "Aminoacid constitution of two gastrins isolated from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 22-101, AND CHARACTERIZATION OF GASTRIN 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Molecular cloning of human gastrin precursor cDNA.";
Gene 26:53-57(1983).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Biochem. Biophys. Res. Commun. 160 1364-1370(1989)
                                                                                                                                                                                             intron contains an Alu sequence.";
Proc. Natl. Acad. Sci. U.S.A. 81:4662-4666(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R.C.;
II.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-67021327; PubMed-5921183;
Bentley P.H., Kenner G.W., Sheppard
"Structures of human gastrins I and
                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE-84272693; PubMed-6087340;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nature 209:583-585(1966).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  big gastrin fragments."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE-Antral mucosa;
              sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 76-92.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 59-68.
                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matsubara K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tarui
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                                                                              secrete hydrochloric acid and the pancreas to secrete its digestive enzymes. It also stimulates smooth muscle contraction and increases blood circulation and water secretion in the stomach
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GASTRIN 71 (COMPONENT I).
GASTRIN 52 (POTENNIAL).
BIG GASTRIN (GASTRIN 34) (COMPONENT II).
GASTRIN (GASTRIN 17) (COMPONENT III).
PYRROLIDONE CARBOXYLIC ACID.
PYRROLIDONE CARBOXYLIC ACID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                              SUBCELLULAR LOCATION: Secreted.

PTM: TWO DIFFERENT PROCESSING PATHWAYS PROBABLY EXIST IN ANTRAL G-CELLS. IN THE DOMINANT PATHWAY PROGASTRIN IS CLEAVED AT THREE SITES RESULTING IN TWO MAJOR BIOACTIVE GASTRINS, GASTRINS, GASTRINS, GASTRINS, GASTRINS, TREE DEFENDANTIVE PATHWAY, PROGASTRIN MAY BE PROCESSED ONLY AT THE MOST C-TERMINAL DIBASIC SITE RESULTING IN THE SYNTHESIS OF GASTRINS-71.

SIMILARITY: BELONGS TO THE GASTRIN/CHOLECYSTOKININ FAMILY.
Zollinger-Ellison tumour tissue.";
Gut 10:603-608(1969).
-!- FUNCTION: Gastrin stimulates the stomach mucosa to produce and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SULFATION (IN 33% OF THE CHAINS).
AMIDATION (G-93 PROVIDE AMIDE GROUP).
PHOSPHORYLATION (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS00259; GASTRIN; 1.
Hormone; Cleavage on pair of basic residues; Amidation; Sulfation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
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Pred. No. 0.068;
1; Mismatches (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-JUL-1986 (Rel. 01, Created)
01-NOV-1991 (Rel. 20, Last Sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL, X00183; CAA25005.1; --
EMBL, X00183; CAA25006.1; --
EMBL, X00183; CAA25007.1; --
EMBL; V00511; CAA23769.1; --
EMBL, M1558; AAA5220.1; --
EMBL; K01254; AAB59533.1; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR001651; Gastrin.
Pfam; PF00918; Gastrin; 1.
SMART; SM00029; GASTRIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11394 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Signal; Phosphorylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genew; HGNC:4164; GAS.
MIM; 137250; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PIR, A01617; GMHUB.
PIR, A18854; A18854.
PIR, A32487.
PIR, B32487.
PIR, B32487.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
**A 8; Conserv?
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               101 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           76 QGPWLEEEE 84
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P01354;
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MOD_RES
MOD_RES
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SEQUENCE
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Eutheria; Primates; Catarrhini; Cercopithecidae;
  Mammalia; Eutheria; Prim
Cercopithecinae; Macaca.
                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Canis familiaris (Dog).
                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-JUL-1986 (Rel. 01,
15-JUL-1998 (Rel. 36,
15-JUN-2002 (Rel. 41,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 96-104.
TISSUE-Antral mucosa;
                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gastrin precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                  and intestine
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                                                                                                                                                                                                                                                                                                                                                                           σ
                                                                                                                                                                                                                                                                                                                                                     1 EGPWLEEEE 9
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                         NCBI_TaxID=9544;
                                                                                                                                                                                                                                                                                                                                                                          1 QGPWMEEEE
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MOD_RES
MOD_RES
SEQUENCE
                                                                                               sednences
                                                SEQUENCE
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GAST_CANFA
                                                                                                                                                                                                                                                                                                                              Matches
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                                                                                                                                                                                                                                                                                                                                                      õ
                                                                                                                                                                                                                                                                                                                                                                           Dp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
0
                                                                                                                                                                                   spectrometry.";
J. Am. Chem. Soc. 91:3096-3097 (1969).
-!- FUNCTION: Gastrin stimulates the stomach mucosa to produce and secrete hydrochloric acid and the pancreas to secrete its digestive enzymes. It also stimulates smooth muscle contraction and increases blood circulation and water secretion in the stomach
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                        PIR; A01621; GMCT.

PIR; S14401; S14401.

PIR: DrerPor, IPR001651; Gastrin.

Pfam; PF00918; Gastrin; 1.

SMART; SM00029; GASTRIN; 1.

PROSITE; PS00259; GASTRIN; 1.

PROSITE; PS00259; GASTRIN; 1.

PROSITE; PS00279; GASTRIN; 1.

PROSITE; PS002791; GASTRIN; 1.

Signal; Phosphorylation.

SIGNAL

1 21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SULFATION (PARTIAL).
AMIDATION (G-93 PROVIDE AMIDE GROUP).
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          Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                     SEQUENCE OF 76-92.
MEDLINE=69206035; PubMed=5784957;
Agarwal K.L., Kenner G.W., Sheppard R.C.;
"Feline gastrin. An example of peptide sequence analysis by mass
                                                                                             and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .,
                                                                                                                                                                                                                                                                 SUBCELLULAR LOCATION: Secreted.
SIMILARITY: BELONGS TO THE GASTRIN/CHOLECYSTOKININ FAMILY.
                                                      SEQUENCE FROM N.A. MEDLINE=92127058; PubMed=1773057; Kim S.J., Uhm K.N., Kang Y.K., Yoo O.J., "Bovine and feline gastrin cDNA sequences and the amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PHOSPHORYLATION (BY SIMILARITY).
4DB92E4416A7AC9F CRC64;
          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Butelec
Mammalia, Eutheria, Carnivora, Fissipedia, Felidae, Felis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 50; DB 1; Length 104; Pred. No. 0.07;
                                                                                                     nucleotide sequence homologies among mammalian species.";
DNA Seq. 1:181-187(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PYRROLIDONE CARBOXYLIC ACID. PYRROLIDONE CARBOXYLIC ACID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BIG GAST
GASTRIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Macaca mulatta (Rhesus macaque).
silvestris catus (Cat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11482 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      94.38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               88.98;
                                                                                                                                                                                                                                                                                                                                                                                              EMBL; X16582; CAA34599.1;
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92
92
95
96
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                                   NCBI_TaxID=9685;
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SEQUENCE OF
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stomach
                          Yu J., Xin Y., Eng J., Yalow R.S.; "Rhesus monkey gastroenteropancreatic hormones: relationship to human
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                                                                                                        Pegul. Pept. 32:39-45(1991).
-!- FUNCTION: Gastrin stimulates the stomach mucosa to produce and secrete hydrochloric acid and the pancreas to secrete its digestive enzymes. It also stimulates smooth muscle contraction and increases blood circulation and water secretion in the stoma
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Carnivora, Fissipedia, Canidae, Canis.
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MEDLINE-91085716; PubMed-2262079;
Gantz I., Takeuchi T., Yamada T.;
"Cloning of canine gastrin cDNA's encoding variant amino acid
                                                                                                                                                                                                                                                                                 -!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: BELONGS TO THE GASTRIN/CHOLECYSTOKININ FAMILY.
PIR; A60071; A60071.
InterPro; INFO01651; Gastrin.
PROSTITE; PS00299; GASTRIN; 1.
HORMONE; Amidation; Sulfation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             PYRROLIDONE CARBOXYLIC ACID.
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6F6E92C73611D39A CRC64;
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Pred. No. 0.024;
; Mismatches
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Agarwal K.L., Kenner G.W., Sheppard R.C.;
"Structure and synthesis of canine gastrin.";
Experientia 25:346-348(1969).
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Last sequence update)
Last annotation update)
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MEDLINE=87016557; PubMed=3763441;
MEDLINE=91164506; PubMed=2003150;
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77.88;
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QGPWMEEEE
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P04564;
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  SYNTHESIS
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                                                                                      and increases blood circulation and water secretion in the stomach and intestine.
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MEDLINE-80240380; PubMed-6930858;
Agarwal K.L., Noyes B.E.;
Studies on gastrin mRNA structure using an oligonucleotide probe.";
Ann. N.Y. Acad. Sci. 343:433-442(1980).
          Desmond H., Varro A., Young J., Gregory H., Nemeth J., Dockray G.J., "The constitution and properties of phosphorylated and unphosphorylated C-terminal fragments of progastrin from dog and
                                     ferret antrum.";
Regul. Pept. 25:223-233(1989).
-!- FUNCTION: Gastrin stimulates the stomach mucosa to produce and secrete hydrochloric acid and the pancreas to secrete its digestive enzymes. It also stimulates smooth muscle contraction
                                                                                                                          Pfam; PF00918; Gastrin.
SMARY; SW00029; GASTRIN; 1.
PROSITE; PS00259; GASTRIN; 1.
PROSITE; PS00259; GASTRIN; 1.
Signal; Phosphorylation.
Signal; Phosphorylation.
                                                                                                                                                                                                                                              SULFATION (PARTIAL).
AMIDATION (G-93 PROVIDE AMIDE GROUP).
PHOSPHORYLATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Suina, Suidae, Sus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-82174533; PubMed-6951161; Yoo O.J., Powell C.T., Agarwal K.L.; Molecular cloning and nucleotide sequence of full-length of cDNA coding for porcine gastrin.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 76-92.
Gregory H., Hardy P.M., Jones D.S., Kenner G.W., Sheppard R.C.;
"The antral hormone gastrin.";
Nature 204:931-933(1964).
                                                                                                                                                                                                                                                                                                                                    ;
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    -!- SUBCELLULAR LOCATION: Secreted.
    -!- SIMILARITY: BELONGS TO THE GASTRIN/CHOLECYSTOKININ FAMILY.
    PIR; JS0425; GMDG.

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                                                                                                                                                                                                                          PYRROLIDONE CARBOXYLIC ACID. PYRROLIDONE CARBOXYLIC ACID.
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                                                                                                                                                                                                       BIG GASTRIN (GASTRIN 34).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                         0.15;
                                                                                                                                                                                                                                                                                                                                                                                                                         104 AA
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2; Mismatches
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MEDLINE-89331947; PubMed-2756156;
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21-JUL-1986 (Rel. 01,
15-JUN-2002 (Rel. 41,
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Best Local Similarity
                                                                                                                                                                                                                                                                                              104 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gastrin precursor.
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76 QGPWMEEEE 84
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P01351;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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                                                                                                                        -:- FUNCTION: Gastrin stimulates the stomach mucosa to produce and secrete hydrochloric acid and the pancreas to secrete its sorted digestive enzymes. It also stimulates smooth muscle contraction and increases blood circulation and water secretion in the stomach and intestine.

-:- SUBCELLULAR LOCATION: Secreted.
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MEDLINE-87016557; PubMed=3763441;
Bonato C., Eng J., Hulmes J.D., Miedel M., Pan Y.-C.E., Yalow R.S.;
"Sequences of gastrins purified from a single antrum of dog and of
Anderson J.C., Barton M.A., Gregory R.A., Hardy P.M., Kenner G.W., McLeod J.K., Preston J., Sheppard R.C., Morley J.S.; "Synthesis of gastrin."; Nature 204:933-934(1964).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS00259; GASTRIN; 1. Hormone; Cleavage on pair of basic residues; Amidation; Sulfation;
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SULFATION (IN 66% OF THE CHAINS).
AMIDATION (G-93 PROVIDE AMIDE GROUP).
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
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01-FEB-1994 (Rel. 28, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
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11558 MW;
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InterPro; IPR001651; Gastrin.
Pfam; PF00918; Gastrin; 1.
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Peptides 7:689-693(1986).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        veen the Swiss Institute of Bioinformatics and the EMBL outstation -
European Bioinformatics Institute. There are no restrictions on its
      contraction in the stomach
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FUNCTION: Gastrin stimulates the stomach mucosa to produce and secrete hydrochloric acid and the pancreas to secrete its digestive enzymes. It also stimulates smooth muscle contraction and increases blood circulation and water secretion in the stomach
                                                                                                                                                                                                                        Gaps
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MEDLINE-68357500; PubMed=5665711;
Agarwal X.L., Beacham J., Bentley P.H., Gregory R.A., Kenner G.W., Shepperd R.C., Tracy H.J.;
"Isolation, structure and synthesis of ovine and bovine gastrins.";
Nature 219:614-615(1968).
                                                                                                Hormone; Cleavage on pair of basic residues; Amidation; Sulfation.
PEPTIDE 1 34 BIG GASTRIN (GASTRIN 34).
                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-92127058; PubMed-1773057; Kim S.J., Uhm K.N., Kang Y.K., Yoo O.J.; "Bovine and feline gastrin cDNA sequences and the amino acid and nucleotide sequence homologies among mammalian species."; DNA Seq. 1:181-187(1991).
and increases blood circulation and water secretion in the and increases blood circulation and water secretion in the and intestine.
--- SUBCELIULAR LOCATION: Secreted.
--- SIMILARITY: BELONGS TO THE GASTRIN/CHOLECYSTOKININ FAMILY. PRIS, JS0426.
Interpro: IPR001651; Gastrin.
PROSTE: PS00918; Gastrin; 1.
HOMMONE: Cleanse.
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                                                                                                                                                                                                Score 47; DB 1; Length 34; Pred. No. 0.071;
                                                                                                                                  PYRROLIDONE CARBOXYLIC ACID.
PYRROLIDONE CARBOXYLIC ACID.
                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lund T., Olsen J., Rehfeld J.F.;
"Cloning and sequencing of the bovine gastrin gene.";
                                                                                                                                                                            67501111E76D0CF4 CRC64;
                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                    104 AA
                                                                                                                                                                                                                      2; Mismatches
                                                                                                                                                      SULFATION
                                                                                                                                                                   AMIDATION
                                                                                                                        GASTRIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mol. Endocrinol. 3:1585-1588(1989).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=90114160; PubMed=2608050;
                                                                                                                                                                                                                                                                                                                                        (Rel. 01, Created)
                                                                                                                                                                                                88.78;
                                                                                                                                                                                                          77.88;
                                                                                                                                                                            3903 MW;
                                                                                                                                                                                                        Local Similarity 77.8
nes 7; Conservative
                                                                                                                                                                                                                                                                                                                    STANDARD;
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18
29
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(Rel. 41, 1
                                                                                                                                                                                                                                                                                                                                                                                                                           Bovidae; Bovinae; Bos.
NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                            taurus (Bovine)
                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                      Gastrin precursor.
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                                                                                                                                                                           34 AA;
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18 QGPWVEEEE 26
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                                                                                                                                                                                                                                                                                                                 GAST_BOVIN ST
P01352, Q28114;
21-JUL-1986 (Rel.
01-NOV-1991 (Rel.
15-JUN-2002 (Rel.
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18
29
34
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                                                                                                                                                                                                                                                                                                                                                                                            Bos taurus
Eukaryota;
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MOD_RES
SEQUENCE
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MOD_RES
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the Euror
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modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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MEDLINE=68357500; PubMed=5665711;
Agarwal K.L., Beacham J., Bentley P.H., Gregory R.A., Kenner G.W.,
Sheppard R.C., Tracy H.J.,
Isolation, structure and synthesis of ovine and bovine gastrins.";
Nature 219:614-615(1968).
    is in
                                                                                                                                                                                                           MO0029; GASTRIN; 1.
PS00259; GASTRIN; 1.
Cleavage on pair of basic residues; Amidation; Sulfation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
Bovidae, Caprinae, Ovis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FUNCTION: Gastrin stimulates the stomach mucosa to produce and
                                                                                                                                                                                                                                                                                                                                                                                                           PROVIDE AMIDE GROUP).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 47; DB 1; Length 104; Pred. No. 0.22;
  as its content
                                                                                                                                                                                                                                                                                                                                                PYRROLIDONE CARBOXYLIC ACID. PYRROLIDONE CARBOXYLIC ACID.
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                                                                                                                                                                                                                                                                                                            BIG GASTRIN (GASTRIN 34).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CRC64;
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N -> T (IN REF. 1).
N -> T (IN REF. 1).
E -> G (IN REF. 1).
E -> G (IN REF. 1).
S -> M (IN REF. 1).
E -> G (IN REF. 1).
S -> M (IN REF. 1).
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S -> M (IN REF. 1).
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AMIDATION (G-93 PROV
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15-JUL-1998 (Rel. 36, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                             PHOSPHORYLATION
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non-profit institutions as long
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                                                                                                                               PIR; B01619; GMBO.
PIR; S14400; S14400.
InterPro; IPR001651; Gastrin.
PFam; PFC0918; Gastrin. 1.
SMART; SM00029; GASTRIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11573 MW;
                                                                                      EMBL; M31657; AAA30537.1; -. EMBL; X16581; CAA34598.1; -.
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                                                                                                                                                                                                                                                                    Signal; Phosphorylation
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927
937
937
944
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Best Local Similarity
7; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ovis aries (Sheep).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   :|||:||||
76 QGPWVEEEE 84
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Pfam; PF01916; DS; 1.
ProDom; PD007730; DS; 1.
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Q9V0N5;
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                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                            Pfam: PF00918; Gastrin; 1.
SMART: SW00029; GASTRIN; 1.
HOROSITE: PS00259; GASTRIN; 1.
HORMONE: Cleavage on pair of pasic residues; Amidation; Sulfation; Signal; Phosphorylation.
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AMIDATION (G-93 PROVIDE AMIDE GROUP).
AMIDATION (G-93 PROVIDE AMIDE GROUP).
624063D4B5CE5AFD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Unique progastrin processing in equine G-cells suggests marginal tyrosyl sulfotransferase activity.";
Eur. J. Biochem. 255:432-438[958].
-i- FUNCTION: Gastrin stimulates the stomach mucosa to produce and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-98380242; PubMed-9716385;
Johnsen A.H., Sandin A., Rourke I.J., Bundgaard J.R., Nilsson G.,
Rehfeld J.F.;
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SUBCELLULAR LOCATION: Secreted. SIMILARITY: BELONGS TO THE GASTRIN/CHOLECYSTOKININ FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 47; DB 1; Length 104; Pred. No. 0.22;
                                                                                                                                                                                                                                                                                                                                                                                                                                              GASTRIN.
PYRROLIDONE CARBOXYLIC ACID.
PYRROLIDONE CARBOXYLIC ACID.
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01-NOV-1997 (Rel. 35, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11532 MW;
                                                                                                                                                                                                                                                                          InterPro; IPR001651; Gastrin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                88.7%;
                                                                                                                                                                                                                                    EMBL; U92801; AAB51307.1; -.
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Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            104 AA;
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and intestine.
                                                                                                                                                                                                                                                          PIR; A01619; GMSH
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P55885;
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MOD_RES
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SEQUENCE
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entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: CATALYZES THE NAD-DEPENDENT OXIDATIVE CLEAVAGE OF
SPERMIDINE AND THE SUBSEQUENT TRANSFER OF THE BUYLLAMINE MOIETY OF
SPERMIDINE TO THE EPSILON-AMINO GROUP OF A SPECIFIC LYSINE RESIDUE
OF THE BIF-5A PRECURSOR PROTEIN TO FORM THE INTERMEDIATE
DEOXYHYPUSINE RESIDUE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Pyrococcus abyssi genome sequence: insights into archaeal chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                         PYRROLIDONE CARBOXYLIC ACID (POTENTIAL).
PYRROLIDONE CARBOXYLIC ACID (POTENTIAL).
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                                                                                                                                                                                                                                PROSITE; PS00259; GASTRIN; 1.

Hormone; Cleavage on pair of basic residues; Amidation; Sulfation; Signal; Phosphorylation.

SIGNAL
PEPTIDE 62 95 GASTRIN (GASTRIN 34).

PEPTIDE 79 95 GASTRIN.

MOD_RES 62 PYRROLIDONE CARBOXYLIC ACID (POTENTIAL MOD_RES 79 79 PYRROLIDONE CARBOXYLIC ACID (POTENTIAL MOD_RES 90 90 SULFATION (PARTIAL).

MOD_RES 95 AMIDATION (G-96 PROVIDE ARIDE GROUP).

MOD_RES 95 PHOSPHORYLATTON (BY SIMILARITY).

SEQUENCE 107 AA, 11884 MW; 104166CAAB5C234F CRC64;
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-:- COFACTOR: NAD (BY SIMILARITY).
-:- PATHWAY: Hypusine biosynthesis; first step.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Probable decxyhypusine synthase (EC 2.5.1.46) (DHS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 46; DB 1;
Pred. No. 0.34;
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                                                                                                                                   InterPro; IPR001651; Gastrin.
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                                                                                                       EMBL; Y09440; CAA70590.1; -
                                                                                                                                                                     Pfam; PF00918; Gastrin; 1.
SMART; SM00029; GASTRIN; 1.
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Best Local Similarity
7; Conserve
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Gaps

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Indels

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Mismatches

2

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6; Conservative
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                                   1 EGPWLEEE
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Q96PE6;
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SEQUENCE
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ZN_FING
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ZN_FING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZN_FING
                                                                                                                   ZIM3_HUMAN
         Matches
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                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb.ch/announce/or send an email to license@isb-sib.ch).
                                                                                      ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Science 273:1058-1073(1996).

-I- FUNCTION: CATALYZES THE NAD-DEPENDENT OXIDATIVE CLEAVAGE OF SPERMIDINE AND THE SUBSEQUENT TRANSFER OF THE BUTYLAMINE MOIETY OF SPERMIDINE TO THE EPSILON-AMINO GROUP OF A SPECIFIC LYSINE RESIDUE OF THE EIF-5A PRECURSOR PROTEIN TO FORM THE INTERMEDIATE DEOXYHYPUSINE RESIDUE (BY SIMILARITY).

-I- CATALYTIC ACTIVITY: [eIF5A-precursor]-lysine + spermidine = [eif5A-precursor]-deoxyhypusine + propane-1,3-diamine.
                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.

STRAIN-JAL-1 / DSM 2661 / ATCC 43067;

MEDLINE-96337999; PubMed-8688087;

Bult C.J., White O., Olsen G.J., Elulu L., Fleischmann R.D.,

Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,

Kerlavage A.R., Dougherty B.A., Tomb J.F., Adams M.D., Reich C.I.,

Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,

Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,

Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,

Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Bordovsky M.,

Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.,

"Complete gnome sequence of the methanogenic archaeon, Methanococcus
                                                                                      Gaps
                                                                                      ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- COFACTOR: NAD (BY SIMILARITY).
-!- PATHWAY: Hypusine biosynthesis; first step.
-!- SIMILARITY: BELONGS TO THE DEOXYHYPUSINE SYNTHASE FAMILY.
dhys; 1.
s; Transferase; NAD; Complete proteome.
a1997 MW; 3DE853F38029EC55 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; Irrocci.
Pfam; PRO1916; DS; 1.
ProDom; PRO1916; DS; 1.
TIGREAMS; TIGR00321; dhys; 1.
Hypusine biosynthesis; Transferase; NAD; Complete proteome.
And And S199781MW; ArrB306337FED7CD CRC64;
                                                        Score 43; DB 1; Length 335;
Pred. No. 3.5;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 42; DB 1; Length 351; Pred. No. 5.4;
                                                                                                                                                                                                                                                                                                                       Archaea; Euryarchaeota; Methanococci; Methanococcales;
                                                                                                                                                                                                                                  01-NOV-1997 (Rel. 35, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Probable deoxyhypusine synthase (EC 2.5.1.46) (DHS).
                                                                                                                                                                                                                                                                                                                                      Methanocaldococcaceae; Methanocaldococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; U67525; AAB98813.1; ALT_INIT.
HSSP; P49366; 1DHS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR002773; DS. " | InterPro; IPR001230; Prenyl_site
 TIGREAMS; TIGRO0321; dhys; 1.
Hypusine biosynthesis; Transfer
SEQUENCE 335 AA; 37997 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     79.28;
75.08;
                                                          81.1%;
77.8%;
                                                                     Best Local Similarity 77.8
Matches 7; Conservative
                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                          Methanococcus jannaschil.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                           1 EGPWLEEEE 9
                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=2190;
                                                                                                                                                                                                                                                                                           OR MJ0814.
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                                                                                                                                                                                                           DHYS_METJA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          jannaschii
                                                           Query Match
                                                                                                                                                                                              DHYS_METJA
    SO SO
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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InterPro: IPR001909; XRAB.
InterPro: IPR000822; Znf_C2H2.
Pfam; PF00096; zf-C2H2; 11.
Pfam; PF00195; KRAB. 1.
PROSITE; PS50805; KRAB: 1.
PROSITE; PS50157; ZINC_FINGER_C2H2_1; 11.
PROSITE; PS50157; ZINC_FINGER_C2H2_2; 11.
Transcription_regulation; Zinc-finger; Metal-binding; Nuclear protein;
                                                                                                                                                                                                                      Gaps
                                                                                                                                       Craniata; Vertebrata; Euteleostomi;
Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 42; DB 1; Length 472; Pred. No. 7.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               755279B78653F286 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .;
                              15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Zinc finger imprinted 3.
472 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C2H2-TYPE.
C2H2-TYPE.
C2H2-TYPE.
C2H2-TYPE.
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C2H2-TYPE.
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C2H2-TYPE.
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PRT;
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                                                                                                                                     Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             54498 MW;
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STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genew; HGNC:16366; ZIM3
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                                                                                                                     Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
7; Conserve
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DOMAIN 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  167
195
223
223
251
279
307
335
363
4419
4419
4412 AA;
                                                                                                                                                                                                       SEQUENCE FROM N.A.
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73

67 PWLEEEE

q

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0
                                                                                                                                                                                        Gaps
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"Chinchilla 'big' and 'little' gastrins.";
Blochem. Blophys. Res. Commun. 143:7-14(1987).
-!- FUNCTION: Gastrin stimulates the stomach mucosa to produce and secrete hydrochloric acid and the pancreas to secrete its digestive enzymes. It also stimulates smooth muscle contraction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chinchilla brevicaudata (Chinchilla).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Hystricognathi; Chinchillidae;
                                                                                                      Cavia porcellus (Guinea pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
                                                                                                                                                                                                                                                                                      -!- SUBCELLULAR LOCATION: Secreted.
                                                                                                                                                                                                                                                                                                                                                           Hormone: Cleavage on pair of basic residues; Amidation PEPTIDE 13 GASTRIN (GASTRIN 33). PEPTIDE 18 33 GASTRIN GASTRIN 33). MOD_RES 18 18 PYRROLIDONE CARBOXYLIC ACID. MOD_RES 18 18 PYRROLIDONE CARBOXYLIC ACID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1; Length 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                               B37C251CD40EB30C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAR-1989 (Rel. 10, Created)
01-MAR-1989 (Rel. 10, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                             01-JAN-1988 (Rel. 06, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                       33 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             33 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 40;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                          AMIDATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'PRT;
                         PRT;
                                                                                                                                                                 SEQUENCE.
MEDLINE-86309993; PubMed-3747718;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE.
MEDLINE-87156784; PubMed-3827930;
                                                                                                                                                                                                                                                                                                              PIR; A26089; GMGPB.
InterPro; IPR001651; Gastrin.
Pfam; PF00918; Gastrin; 1.
PROSITE; PS00259; GASTRIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          75.5%;
75.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                          33
3757 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD; ,
                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 75.v.
6; Conservative
                       STANDARD;
                                                                                                                                                                                                                                                                             and intestine.
                                                                                                                                                                                                                                                                                                                                                                                                                                    33 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chinchilla.
NCBI_TaxID=10152;
                                                                                                                                            NCBI_TaxID=10141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      :111 | 11
18 QGPWAEEE 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 EGPWLEEE 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Big gastrin.
GAS.
                                                                                 Big gastrin.
GAS.
                      GAST_CAVPO
P06885;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GAST_CHIBR
P10034;
                                                                                                                                                                                                                                                                                                                                                                                               MOD_RES
MOD_RES
MOD_RES
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 15
GAST_CHIBR
RESULT 14
GAST_CAVPO
                         ô
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0;
and increases blood circulation and water secretion in the stomach and intestine.
                                                                                                                          Gaps
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0
                                                                                                             Length 33;
                                                                           PYRROLIDONE CARBOXYLIC ACID. SULFATION.
                                                                                                                        1; Indels
                                                                BIG GASTRIN (GASTRIN 33)
GASTRIN.
                                                                                         AMIDATION.
6F11F5CDC50FAA2D CRC64;
                                                                                                            DB 1;
                                                                                                                         Mismatches .
                                                                                                            Score 40;
Pred. No. 3
                                                                                                            75.5%;
                                                                                               3715 MW;
                                                                                                                          Conservative
                                                                        33
18
28
33
                                                                                                                   Similarity
                                                                                                33 AA;
                                                                                                                                             :||| |||
18 QGPWAEEE 25
                                                                                                                                     1 EGPWLEEE 8
                                                                                                                          9
                                                                PEPTIDE
PEPTIDE
MOD_RES
MOD_RES
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                                                                                                             Query Match
Best Local :
                                                                                                                          Matches
  qq
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Search completed: February 5, 2003, 09:48:17 Job time : 7.42857 secs

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February 5, 2003, 09:45:51; Search time 21 Seconds (without alignments) 88.306 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                             671580
GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                       671580 segs, 206047115 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                  Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                    OM protein - protein search, using sw model
                                                                                                                                                                                                                                                  BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sp_archea:*
sp_bacteria:*
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53
1 EGPWLEEEE 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SPTREMBL_21:*
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

sp\_unclassified:\*

sp\_virus:\*
sp\_vertebrate:\*

sp\_organelle:\*
sp\_phage:\*

sp\_plant:\* sp\_rodent:\*

sp\_rvirus:\*
sp\_bacteriap:\*
sp\_archeap:\*

	Description	09scpl arabidopsis		08x4r9 escherichia		8	9	0									
SUMMARIES	DI	Q9SCP1	088415	Q8X4R9	Q941F9	Q941F8	Q94IF6	03 <b>x</b> 20	Q93V46	039028	049020	Q94JN5	Q94JN4	P81394	Q9FJP2	09C0D5	Q8VE83
	DB	10	10	16	10	10	10	10	10	10	10	10	10	10	10	11	11
	Query Match Length DB	238	160	248	273	273	273	273	273	273	293	293	293	268	310	311	311
æ	Query	84.9	77.4	77.4	77.4	77.4	77.4	77.4	77.4	77.4	77.4	77.4	77.4	75.5	75.5	75.5	75.5
	Score	45	41	41	41	41	41	41	41	41	41	41	41	40	40	40	40
	Result No.	1	7	æ	4	5	9	7	89	6	10	11	12	13	14	15	16

; 0

Gaps

.; 0

Query Match 84.9%; Score 45; DB 10; Length 238; Best Local Similarity 87.5%; Pred. No. 7.8; Matches 7; Conservative 1; Mismatches 0; Indels

PG8 0618 0618 0618 0618 0618 0618 0618 0701 0701 0701 0701 0701 0701 0701 07	O98pg8 arabidopsis O23618 arabidopsis O82065 peanut stun O82118 pyrobaculum O84000 oryza sativ O8W000 oryza sativ O8W100 mus musculu O31208 mus musculu O31206 mus musculu O34701 oryza sativ O64704 dromo sapien O8416 zea mays (m O6603 arabidopsis O9604 arabidopsis O9604 arabidopsis O9605 arabidopsis O91208 arabidopsis	NTS	13, Created) 13, Last sequence update) 20, Last annotation update) 20, Last annotation update) 21, Last sequence update) 22, Last annotation update) 23, Last sequence update) 24; Streptophyta; Embryophyta; Tracheophyta; 25; Streptophyta; Embryophyta; Rosidae; 26; Streptophyta; Embryophyta; Rosidae; 27; Brassicaceae; Arabidopsis. 28; Brassicaceae; Arabidopsis. 31, Dauner D., Sterr W., Holland R., 28; H.W., Lemcke K., Mayer K.F.X., Quetier F., 32, Dauner D., Sterr W., Holland R., 33, Dauner D., Sterr W., Holland R., 34, Dauner D., Sterr W., Holland R., 35, Dauner D., Sterr W., Holland R., 36, Dauner D., Sterr W., Holland R., 37, Dauner D., Sterr W., Holland R., 38, Dauner D., Sterr W., Holland R., 39, Dauner D., Sterr W., Holland R., 31, Dauner D., Sterr W., Holland R., 32, MYB-LIKE DOMAINS. 31, Dauner D., Sterr W., Holland R., 31, Dauner D., Sterr W., Holland R., 32, Dauner D., Sterr W., Holland R., 33, Dauner D., Sterr W., Holland R., 34, Dauner D., Sterr W., Holland R., 35, Dauner D., Sterr W., Holland R., 36, Dauner D., Sterr W., Holland R., 37, Dauner D., Sterr W., Holland R., 38, Dauner D., Sterr W., Holland R., 39, Dauner D., Sterr W., Holland R., 31, Dauner D., Sterr W., Holland R., 32, Dauner D., Sterr W., Holland R., 33, Dauner D., Sterr W., Holland R., 34, Dauner D., Sterr W., Holland R., 36, Dauner D., Sterr W., Holland R., 37, Dauner D., Sterr W., Holland R., 38, Dauner D., Sterr W., Holland R., 39, Dauner D., Sterr W., Holland R., 30, Dauner D., Sterr W., Holland R., 31, Dauner D., Sterr W., 31, Dauner D., Sterr W., 31, Dauner D., 32, Dauner D., 33, Dauner D., 34, Dauner D., 35, Dauner D., 36, Dauner D., 37, Dauner D., 38, Dauner D., 38, Dauner D., 38, Dauner D., 39, Dauner D., 30, Dauner D., 30, Dauner D., 30, Dauner D., 30, Dauner D., 31, Dauner D., 31, Dauner D., 31, Dauner D., 32, Dauner D., 33, Dauner D., 34, Dauner D., 35, Dauner D., 36, Dauner D., 37, Dauner D., 38, Dauner D., 38, Da
	09SPG8 023618 082065 082118 031205 08W0D5 08BCZ1 08BCZ1 08W4D9 031206 0947V1 0947V1 0947V1 0947V1 0947V1 0947V1 095009 022214 095009 095009 095009 095009 095009 095009 095009	ALIGNMENT	Created) Last sequence ul Last sequence ul Last annotationear cress) treptophyta; Emb. a; eudicotyledon brassicaceae; Aral rassicaceae; Aral
	100 110 120 170 170 170 170 170 170 170 170 170 17		; 113, 20, 20, 20, 20, 20, 31, Br the the the the the the the the the the
10 10 10 10 10 10 10 10 10 10	2220 244 244 254 254 254 254 254 254		MINARY BELrel. BELrel. BELrel. Belrel. Complementation of the plantation of the plan
MINARY; BLrel. 13, BLrel. 13, BLrel. 13, BLrel. 13, BLrel. 13, Britan B. C  1, Mewes H.  1, Mewe	755.55 772.77		PRELLI (TIPE (TIPE (TIPE IN III II
75.5 349 10 75.5 349 10 75.5 349 10 75.5 834 12 73.6 181 17 73.6 304 7 73.6 304 7 73.6 344 7 73.6 344 7 73.6 379 7 73.6 379 7 73.6 379 7 73.6 108 10 73.7 18 10 73.6 108 10 73.7 18 10 73.6 108 10 73.6 108 10 73.6 108 10 73.6 108 10 73.6 108 10 73.7 235 10 73.7 235 10 73.7 235 10 73.7 235 10 73.7 235 10 73.7 236 10 73.7 238 10 73.7 240 10 73.8 20 10 73.8	4 4 4 6 6 6 6 6 6 6 7 7 8 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9	·	SCP1MAY-2000MAY-2000MAY-2000MAY-2000MAY-2000MAY-2000
10	11112222222222222222222222222222222222	E C	RESULT  O995CP1  O905CP1  O010  DT  O010

28619 MW; DOF452DA2299E3D8 CRC64;

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EMBL; AP002562; BAB37034.1;
            Complete proteome. SEQUENCE 248 AA;
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Q941F8;
                                                                                                                                                                         Q94 IF9;
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                                                                 Matches
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  SO KW
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                                                                                                                                                  Zea mays (Maize).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; PACC clade;
Panicoideae; Andropogoneae; Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-21156231; PubMed=11258796;
MEDLINE-21156231; PubMed=11258796;
MEDLINE-21156231; PubMed=11258796;
MEDLINE-21156231; PubMed=11258796;
Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,
Kuhara S., Shiba T., Hattori M., Shinagawa H.;
"Complete genome sequence of enterohemorrhagic Escherichia coli
O157:H7 and genomic comparison with a laboratory strain K-12.";
EMBL; AE005503; AAG57864.1; -.
                                                                                                                                                                                                                                                                                                                 Gaps
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MEDLINE-21074935, PubMed-11206551;
MEDLINE-21074935, PubMed-11206551;
MEDLINE-21074935, PubMed-11206551;
Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
Posfal G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
Welch R.A., Blattner F.R.;
"Genome sequence of enterchaemorrhagic Escherichia coli 0157:H7.";
Nature 409:529-533(2001).
                                                                                                                                                                                                                      Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
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                                                                                                                                                                                                                                                                                           Length 160;
                                                                                                                                                                                                                                                                                                                1; Indels
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
11-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Orf, hypothetical protein.
24066 OR ECS3611.
                                                                                                         Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                         Score 41; DB 10;
Pred. No. 24;
2; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                              248 AA
                                                                                                Created)
                                                                          PRT;
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Best Local Similarity 6b./.
6, Conservative
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                                                                         PRELIMINARY;
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                                                                                                                01-JUN-2002 (TrEMBLrel. P-type R2R3 Myb protein. MYB49.
                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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15 KGPWTEEED 23
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             1 EGPWLEEEE 9
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2 GPWLEEEE 9
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Q8X4R9
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                                                        Gaps
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Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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"Nucleotide polymorphism at the Atmyb2 locus of the wild plant
Arabidopsis thaliana.";
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Kamiya T., Kawabe A., Miyashita N.T.;
"Nucleotide polymorphism at the Atmyb2 locus of the wild plant
Arabidopsis thaliana.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       77.4%; Score 41; DB 10; Length 273; 66.7%; Pred. No. 40; 1; Indels Live 2; Mismatches 1; Indels
  Length 248;
                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                      01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
MYB transcription factor Atmyb2.
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PROSITE; PS00063; ALDOKETO_REDUCTASE_3; UNKNOWN_1
PROSITE; PS00037; MYB_1; UNKNOWN_1.
PROSITE; PS00334; MYB_2; UNKNOWN_1.
                                                        1;
  77.4%; Score 41; DB 16; 66.7%; Pred. No. 37;
                                                                                                                                                                                                                                                                                                    273 AA
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                                                     2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Arabidopsis thaliana (Mouse-ear cress).
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InterPro; IPR001395; Aldo/ket_red.
InterPro; IPR01005; Myb_DNA_binding.
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                                                          Conservative
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nes 6; Conservative
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Query Match
Best Local Similarity
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234 QGPWLSKEE 242
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SEQUENCE_FROM N.A.
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                                                                                                             1 EGPWLEEEE 9
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Arabidopsis thaliana (Mouse-ear cress).
Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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T. Kantya T. Kawabe A., Miyashita N.T.;

"Nucleotide polymorphism at the Atmyb2 locus of the wild plant
T. Arabidopsis thallana.";

Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.

R EMBL; AB05244; BAB62129.1;

R EMBL; AB05244; BAB62124.1;

R InterPro: IPR001395; Aldo/ket_red.

R InterPro: IPR001005; Myb_DNa_binding.

R PROSITE; PS00063; ALDOKETO_REDUCTASE_3; UNKNOWN_1.

R PROSITE; PS00033; MYB_1: UNRNOWN_1.

R PROSITE; PS00093; MYB_2: UNKNOWN_1.
                                              SEQUENCE FROM N.A.
STRAIN=VARIOUS STRAINS;
Kamiya T., Kawabe A., Miyashita N.T.;
Nucleotide polymorphism at the Atmyb2 locus of the wild plant
Arabidopsis thaliama.";
Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AB052250; BAB62130.1; -.
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro: IPR001395; Aldo/ket_red.
InterPro: IPR001395; Aldo/ket_red.
InterPro: IPR001005; Myb_DNa_binding.
PROSITE; PS00063; ALDOKETO_REDUCTASE_3; UNKNOWN_1.
PROSITE; PS00003; MYB_1; UNKNOWN_1.
PROSITE; PS000334; MYB_2; UNKNOWN_1.
PROSITE; PS50090; MYB_3; 2.
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EMBL, AB052232, BAB62112.1;
EMBL, AB052233, BAB62113.1;
EMBL, AB052236, BAB62113.1;
EMBL, AB052240, BAB62117.1;
EMBL, AB052240, BAB62120.1;
EMBL, AB052242, BAB62123.1;
EMBL, AB052242, BAB62123.1;
EMBL, AB052244;
EMBL, AB052241;
EMBL, AB052244;
EMBL, AB052241;
EMBL, AB052
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STRAIN=WS-0, KAS-1, AND OST-0;
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Best Local Similarity 66.,",
".has 6; Conservative
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Best Local Similarity 66.7
Matches 6; Conservative
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22 KGPWTEEED 30
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    NCBI_TaxID=3702;
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brasslcales; Brassicaceae; Arabidopsis.
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"Nucleotide polymorphism at the Atmyb2 locus of the wild plant
T Arabidopsis thaliana.";
T Arabidopsis thaliana.";
Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.

R EMBL, AB05239; BAB62119.1;
R InterPro: IPR001305; Aldo/ket_red.
R InterPro: IPR001005; Myb_DNa_binding.
R Pfan: PF00249; myb_DNa_binding. 2
R PROSITE; PS000037; MYB_1: UNRNOWN_1.
R PROSITE; PS00034; MYB_1: UNRNOWN_1.
R PROSITE; PS00090; MYB_2: UNRNOWN_1.
R PROSITE; PS00090; MYB_3: 2.
SEQUENCE 273 AA; 31433 MW; 726186432287049E CRC64;
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(DEC-2000) to the EMBL/GenBank/DDBJ databases,
             EMBL; AB051235; BAB61115.1; -
InterPro; IPR001395; Aldo/ket_red.
InterPro; IPR001005; Myb_nNa_binding.
Pfam; PF000149; Myb_nNa_binding.
Pfam; PF000149; Myb_DNA_binding.
PROSITE; PS00063; ALDOKETO_REDUCTASE_3; UNKNOWN_1.
PROSITE; PS00334; MYBL_1; UNKNOWN_1.
PROSITE; PS00334; MYBL_2; UNKNOWN_1.
SEQUENCE 273 AA; 31429 MW; 52B5D2466790B9E6 CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
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Pred. No. 40;
2; Mismatches 1
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66.78;
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Best Local Similarity 66.7-
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22 KGPWTEEED 30
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22 KGPWTEEED 30
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  Submitted
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Q93VZ0
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SEQUENCE
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Rounsley S.D., Lin X., Ketchum K.A., Crosby M.L., Brandon R.C.,
Spriggs T.A., Mason T.M., Kerlavage A.R., Adams M.D., Somerville C.R.,
                                                                                                                                                                                                                                                                                            Arabidopsis thaliana (Mouse-ear cress).
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales, Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-COLUMBIA;
MEDLINE-94146551; PubMed-8312738;
Urao T., Yamaquchi-Shinozaki K., Urao S., Shinozaki K.;
"An Arabidopsis myb homolog is induced by dehydration stress and its
gene product binds to the conserved MYB recognition sequence.";
Plant Cell 5:1529-1539(1993).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     94BAE5F38C3854DF CRC64;
                                                                                                                                                                                           01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NAR-2002 (TrEMBLrel. 20, Last annotation update)
ATWWIB2 (WYB transcription factor ATWYB2).
MYB2 OR T08113.3 OR ATWYB2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE: PS00063; ALLOKETO REDUCTASE_3; UNKNOWN_1.
PROSITE: PS00037; MYB_1; UNKNOWN_1.
PROSITE: PS00034; MYB_2; 1.
PROSITE: PS50090; MYB_3; 2.
DNA-binding; Nuclear protein.
SEQUENCE 273 AA; 31448 MW; 94BAE5F38C3854DF CF
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                                                                                                                                                          PRT;
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Best Local Similarity 66.7
Matches 6; Conservative
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TRANSFAC; T02536; -
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22 KGPWTEEED 30
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                    1 EGPWLEEEE 9
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                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Venter J.C.;
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Q39028
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Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, Rosidae,
                                                                                                                                                            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Malvales; Malvaceae; Gossypium.
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                                                                                                                                                                                                                                                                                                                              STRAIN=CV. ACALA SJ-2; TISSUE=OVULE;
Loguercio L.L., Zhang J., Wilkins T.A.;
Structure and expression of six classes of myb-domain genes in allotetraploid cotton (Gossypium hirsutum L.).";
Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
-: SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
-: SUBLELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
-: SIMILARITY: CONTAINS 2 MYB-LIKE DOMAINS.
EMBL; AF034133; AAC04719.1; -.
HSSP; P06876; 1MSE.
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STRAINS-CV. LANDRACE 'PALMERI';
STRAINS-CV. LANDRACE 'PALMERI';
"Cronn R., Cedroni M., Haselkorn T., Osborne C., Wendel J.F.;
"PCR-mediated recombination in a polyploid plant.";
"PCR-mediated recombination to a polyploid plant.";
Submitted (MAX-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AF377316; AAR57698 1; -
InterPro; IPR01005; Myb_DNA_binding.
PROSITE: PS00037; MYB_1; UNKNOWN_1.
PROSITE: PS00334; MYB_2; UNKNOWN_1.
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SEQUENCE 293 AA; 33746 MW; 06901890BD174772 CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Myb-like transcription factor Myb 5.
                            Last sequence update)
Last annotation update)
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66.7%; Pred. No. 43;
tive 2; Mismatches 1
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NCBL_TaxID=3635;
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Pfam: PF00249; myb_DNA-binding; 2.
SMART; SM00395; SAMT; 2.
PROSITE; PS00037; MYB_1; UNKNOWN_1.
PROSITE; PS00034; MYB_2; 1.
PROSITE; PS50090; MYB_3; 2.
                                                                                  MYB-like DNA-binding domain protein.
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                                                                                                                                           Gossypium hirsutum (Upland cotton).
01-JUN-1998 (TrEMBLrel. 06, 01-JUN-1998 (TrEMBLrel. 06, 01-MAR-2002 (TrEMBLrel. 20,
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Best Local Similarity
6; Conserve
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SEQUENCE FROM N.A.
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22 KGPWTEEED 30
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23 KGPWTEEED 31
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Query Match
Best Local Similarity 66.70,
Best Local 6; Conservative
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  61
102
                                             268 AA;
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                                                                                                                Best Local Similarity
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Q9FJP2
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STRAIN=J1:522; TISSUE=FLOWER BUDS;
MEDLINE=93005689; PubMed=1840903;
Jackson D., Culianez-Macia F., Prescott A.G., Roberts K., Martin C.;
TExpression patterns of may genes from Antirrhinum flowers.";
Plant Cell 3:115-125(1991).
--- FUNCTION: MAY BE A TRANSCRIPTIONAL ACTIVATOR.
--- TISSUE SPECIFICITY: ROOF, STEM, LEAF, SEED POD, IMMATURE FLOWER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Antirrhinum majus (Garden snapdragon).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Lamiales; Veronicaceae; Antirrhinum.
                                                                                                                                                                                                                                                                                                                            P SEQUENCE FROM N.A.

STRAIN=CV. LANDRACE 'PALMERI';

A Cronn R., Cedroni M., Haselkorn T., Osborne C., Wendel J.F.;

RT Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.

BL Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.

DR EMBL, AF377317; AAK57699.1;

DR InterPro; IPR001005; Myb_DNA_binding.

DR PEROSITE; PS00037; MYB_L; UNKNOWN_1.

DR PROSITE; PS00034; MYB_2; UNKNOWN_1.

DR PROSITE; PS00034; MYB_3; 2.

"FOURTH PROSITE; PS0009; MYB_3; 2.
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TRANSFAC; T02927; ...
InterPro: IPR001005; Myb_DNA_binding.
Pfam; PF00249; myb_DNA-binding; 2.
SMART; SM00395; SANT 1; 2.
PROSITE; PS000334; MYB_1; 1.
PROSITE; PS000334; MYB_1; 2.
PROSITE; PS00034; MYB_3; 2.
Nuclear protein; DNA-binding; Repeat; Transcription regulation.
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                                                                                                                           01-DEC-2001 (TrEMBLrel. 19, Crpated)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Myb-like transcription factor Myb 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         268 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Created)
                                                                                       PRT;
                                                                                                                                                                                                                     Gossypium hirsutum (Upland cotton)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUN-1998 (TrEMBLrel. 06, 01-JUN-1998 (TrEMBLrel. 06, 01-MRR-2002 (TrEMBLrel. 20, MYB-related protein 315. MYB 315.
                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PIR; JQ061; JQ0961.
HSSP; Q03237; 1A5J.
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23 KGPWTEEED 31
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                                                                                    Q94JN4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P81394
                                         RESULT 12
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                                                             Q94JN4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P81394
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Arabidopsis thaliana (Mouse-ear cress).
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brasslcales; Brasslcaceae; Arabidopsis.
                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kotani H., Nakamura Y., Sato S., Asamizu E., Kaneko T., Miyajima N., Tabata S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse).
Sukaryota: Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia: Eutheria: Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Structural analysis of Arabidopsis thaliana chromosome 5. VI. Sequence features of the regions of 1,367,185 bp covered by 19 physically assigned Pl and TaC clones.";

DNA Res. 5.203-216(1988).

-! SIMCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).

-! SIMLARITY: CONTAINS 2 MYB-LIKE DOMAINS.

EMBL; AB013395; BAB11659.1;

-InterPro: IPR001005; MYB_DNA_binding.
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                                                                                                       Length 268;
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                                                                                                                                                             Indels
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                                                  886C04A4F45D26D1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-WAR-2001 (TrEMBLrel. 16, Created)
01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
4930413022Rik protein.
                                                                                                  Score 40; DB 10;
Pred. No. 58;
1; Mismatches 1
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                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
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MYB.
                            MYB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00249; myb_DNA-binding;
SMART; SM00395; SANT; 2.
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PROSITE; PS50090; MYB_3; 2.
DNA-binding; Nuclear protein.
SEQUENCE 310 AA; 35136 MW;
                                                  31110 MW;
                                                                                                     75.5%;
75.0%;
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MEDLINE-21085660; PubMed-11217851;

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RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Arawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Golobori T., Bono H., Rasukawa T., Saito R.,
RA Saito T., Okazaki Y., Golobori T., Bono H., Rasukawa T., Saito R.,
RA Fielschmann W., Casaterland T., Gissi C., King B., Kochiwa H.,
RA Kuchi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Gariboldi M.,
RA Schriml L.M., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Braka J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brake J., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
R Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Sasaki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Haysahlzaki Y.;
RH Haysahlzaki Y.;
RR "Functional annotation of a full-length mouse cDNA collection.";
RME FRBI: AKO13065; BAB28730.1: ---
BOR ERBI: AKO13065; BAB2830.1: ---
BOR SEQUENCE 311 AA; 32630 MW; 9B571209DB5E91C5 CRC64;
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Best Local Similarity 66.7
Matches 6; Conservative
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Search completed: February 5, 2003, 09:49:14 Job time: 22 secs

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NAME/KEY: MOD_RES
LOCATION: (1)
                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Unknown
                                                                                                                                                                                                                                                                                                     PCT-US99-10734-7
LENGTH: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
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                                          : Search time 117 Seconds
(without alignments)
49.595 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1
                                                                                                                                                                                          /cgn2_6/ptgdata/1/paa/US098_COMB.pep:*/cgn2_6/ptgdata/1/paa/US099_COMB.pep:*/cgn2_6/ptbdata/1/paa/US100_COMB.pep:*/cgn2_6/ptcdata/1/paa/US101_COMB.pep:*/cgn2_6/ptcdata/1/paa/US102_COMB.pep:*/cgn2_6/ptcdata/1/paa/US102_COMB.pep:*/cgn2_6/ptcdata/1/paa/US60_COMB.pep:*
     GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     PCT-US99-10734-7
PCT-US99-10751-1
US-08-798-423-7
US-09-700-329-1
US-09-700-378-7
US-09-700-402-1
                                                                                                                                 Total number of hits satisfying chosen parameters:
                                                                                                                     4569144 segs, 644733110 residues
                                                                                                                                                                                                                                                                                                                                                                                                                      SUMMARIES
                                            5, 2003, 09:48:26
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Maximum Match 100%
Listing first 45 summaries

    protein search, using sw model

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Gapop 10.0 , Gapext 0.5
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length: 2000000000
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53
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Match Length
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Sequence 6, Appli
Sequence 60, Appli
Sequence 422, Appli
Sequence 75, Appl
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Sequence 74, Appl
Sequence 74, Appl
Sequence 74, Appl
Sequence 10, Appl
Sequence 12, Appl
Sequence 69, Appl
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Sequence 69, Appli
Sequence 67, Appli
Sequence 196, Appli
Sequence 196, Appli
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Sequence 100, Appl
Sequence 100, Appl
Sequence 99, Appl
Sequence 95, Appl
Sequence 95, Appl
Sequence 7, Appli
Sequence 1756, Ap
Sequence 4, Appli
                                    Sequence 10, Appl
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APPLICANT: Grimes, Stephen
APPLICANT: Grimes, Stephen
APPLICANT: Grimes, Stephen
APPLICANT: Michaell, Dov
APPLICANT: Aphton Corporation
TITLE OF INVENTION: Method for the Treatment of Gastroesophageal Reflux
TITLE OF INVENTION: Disasse
FILE REFERENCE: ACGIPCT
CURRENT APPLICATION NUMBER: PCT/US99/10734
CURRENT FILING DATE: 1999-05-14
EARLIER APPLICATION NUMBER: 60/085,610
 Sequence 1, P
Sequence 10,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    human or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: Description of Unknown Organism: OTHER INFORMATION: synthetic peptide
                                                                                                                                    PCT-US94-04832A-75
US-08-488-320A-75
US-08-488-320A-74
US-08-68-34-546-10
US-08-634-546-11
US-08-634-546-12
US-08-634-546-12
US-08-648-320A-69
US-08-488-320A-69
US-08-488-320A-69
US-08-488-320A-196
US-08-488-320A-196
US-08-648-320A-196
US-08-648-320A-109
US-08-488-320A-109
US-08-488-320A-109
US-08-488-320A-109
US-08-488-320A-109
US-08-488-320A-109
US-08-488-320A-99
US-08-488-320A-99
US-08-488-320A-95
US-08-798-423-1
US-09-506-854-10
US-10-016-306-10
US-08-798-423-6
PCT-US02-22821-60
US-08-529-095-2
US-09-657-276-422
US-10-197-954-60
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US-60-195-053-1756
US-60-163-123-1073
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 7, Application PC/TUS9910734 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EARLIER FILING DATE: 1998-05-15
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 7
   8
1
10
27
27
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9; Conservative
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US-09-700-329-1
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           Matches
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TITLE OF INVENTION: Prevention and Treatment of Hypergastrinemia FILE REPERENCE: 1102865-0035
CURRENT APPLICATION NUMBER: PCT/US99/10751
CURRENT FILING DATE: 1999-05-14
EARLIER APPLICATION NUMBER: US[60/085,714
EARLIER FILING DATE: 1999-05-15
NUMBER OF SEQ ID NOSE: 1990-05-15
SOFTWARE: PATENTIN Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Methods for the Treatment of
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                                                   Length D
                                            100.0%; Score 53; DB 1; 1
100.0%; Pred. No. 4.2e+06;
tive 0; Mismatches 0;
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Best Local Similarity 100.0%; Pred. No. 4.2e+06;
Matches 9; Conservative 0; Mismatches 0;
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Pred. No. 4.2e+06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Gevas, Philip C.
APPLICANT: Gevas, Philip C.
APPLICANT: Gevas, Philip C.
APPLICANT: Gevas, Stephen L.
APPLICANT: Gines, Stephen C.
APPLICANT: Michaeli, Dov
APPLICANT: Macson, Susan A.
TITLE OF INVENTION: Immunological Methods for TITLE OF INVENTION: Gastrointestinal Cancer FILE REFERENCE: 110286-0031
CURRENT APPLICATION NUMBER: 62/08/798,423
CURRENT FILING DATE: 1997-02-07
PRIOR APPLICATION NUMBER: 60/011,411
PRIOR APPLICATION NUMBER: 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 . LOCATION: (1)
. OTHER INFORMATION: Pyroglutamic acid residue
US-08-798-423-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCATION: (1)
COTHER INFORMATION: pyroglutamic acid
PCT-US99-10751-1
                                                                                                                                                                                                                                                                                          Sequence 1, Application PC/TUS9910751 GENERAL INFORMATION:
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                                            Query Match 100.
Best Local Similarity 100.
Matches 9; Conservative
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
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PCT-US99-10734-7
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US-08-798-423-7
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LENGTH: 9
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...cricant Geras, Philip

APPLICANT: Stephen, Grimes
APPLICANT: Stephen, Grimes
APPLICANT: Michael, Dov
TITLE OF INVENTION: Method for the Treatment of Gastroesophageal Reflux Disease
FILE REFERENCE: ACG1USA
CURRENT APPLICATION NUMBER: US/09/700,378
CURRENT FILING DATE: 2000-11-14
PRIOR APPLICATION NUMBER: PCT/US99/10734
PRIOR APPLICATION NUMBER: PCT/US99/10734
PRIOR FILING DATE: 1999-05-14
SPRIOR FILING DATE: 1999-05-15
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin T
LEBNORM:
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   Gaps
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APPLICANT: Gevas, Stephen
APPLICANT: Grimes, Stephen
APPLICANT: Mair Stephen
APPLICANT: Michaeli, Dow
APPLICANT: Watson, Susan
TITLE OF INVENTION Prevention and Treatment of Hypergastrinemia
FILE REFERENCE: ACG20SA
CURRENT APPLICATION NUMBER: US/09/700,329
CURRENT FILING DATE: 2001-02-08
PRIOR RILING DATE: 1999-05-14
PRIOR FILING DATE: 1999-05-15
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patentin version 3.0
SEQ ID NO 1
LENTH: 9
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   Indels
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Mismatches
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COTHER INFORMATION: pyroglutamic acid
US-09-700-329-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            . LOCATION: (1)..(1)
; OTHER INFORMATION: pyroglutamic acid
US-09-700-378-7
                                                                                                                                                                  Sequence 1, Application US/09700329 GENERAL INFORMATION:
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ORGANISM: human gastrin peptide
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Best Local Similarity 100.
Matches 9; Conservative
                                                            FGPWLEEEE 9
                                   1 EGPWLEEEE 9
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Sequence 10, Application US/10016306
Sequence 10, Application US/10016306
GENERAL INFORMATION:
APPLICANT: Cheny, Jill
Lasky, Laurence A.
TITLE OF INVENTION: A NOVEL KAPPA/MU-LIKE PROTEIN TYROSINE
PHOSPHATASE, PTP LAMBDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
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ADDRESSEE: FLEHR HOHBACH TEST ALBRITTON & HERBERT LLP
                                                                                                                                                                                                     APPLICANT: Cheng, Jill
APPLICANT: Lasky, Laurence A.
TITLE OF INVENTION: A NOVEL KAPPA/MU-LIKE PROTEIN TYROSINE
TITLE OF INVENTION: PHOSPHATASE, PTP LAMBDA
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS.
ADDRESSEE: FLEHR HOHBACH TEST ALBRITTON & HERBERT LLP
STREET: 4 Embarcadero Center, Suite 3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 12;
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compartible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 53; DB 19;
100.0%; Pred. No. 0.37;
:ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: A-63478-4/DAV
TELECOMMUNICATION: TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/991,953

FILING DATE: 16-DEC-1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/652,971

FILING DATE: 24-MAY-1996

ATTORNEY/AGENT INFORMATION:

NAME: Vance, DOILY A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC conpatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/506,854
FILING DATE: 17-FEB-2000
                                                                                                                                      US-09-506-854-10; Sequence 10, Application US/09506854; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       39,054
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CITY: San Francisco
STATE: California
COUNTRY: United States
ZIP: 94111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ 1D NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
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Best Local Similarity 100.

Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: protein
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                            1 EGPWLEEEE 9
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GENERAL INFORMATION:
APPLICANT APHTON CORPORATION
TITLE OF INVENTION: Combination Therapy for the Treatment of Tumors
FILE REFERENCE: 1102865-0034
CURRENT APPLICATION NUMBER: US/09/700,402
CURRENT APPLICATION NUMBER: US/09/700,402
PRIOR APPLICATION NUMBER: US/09/700,402
PRIOR FILING DATE: 1998-05-15
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1
LENGTH: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Gevas, philip C.
APPLICANT: Grans, stephen L.
APPLICANT: Grimes, Stephen L.
APPLICANT: Grimes, Stephen C.
APPLICANT: Michael, Down S.
APPLICANT: Michael, Down S.
TITLE OF INVENTION: Immunological Methods for the Treatment of TITLE OF INVENTION: Immunological Methods for the Treatment of TITLE OF INVENTION: Immunological Methods for the Treatment of FILE REFERENCE: 1102865-0031
CURRENT FILING NUMBER: US/08/T798,423
CURRENT FILING DATE: 1997-02-07
PRIOR APPLICATION NUMBER: 60/011,411
PRIOR APPLICATION NUMBER: 60/011,411
NUMBER OF SEO ID NOS: 8
SOFTWARE: PatentIn Ver. 2.1
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    Length 9;
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100.0%; Score 53; DB 21;
100.0%; Pred. No. 4.2e+06;
iive 0; Mismatches 0;
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Best Local Similarity 100.0%; Pred. No. 4.2e+06;
Matches 9; Conservative 0; Mismatches 0;
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; OTHER INFORMATION: Pyroglutamic acid residue
US-08-798-423-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; NAME/KEY: MOD_RES
; LOCATION: (1)
; COTHER LIOPENATION: pyroglutamic acid
US-09-700-402-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: human or synthetic peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1, Application US/08798423 GENERAL INFORMATION:
                     Best_Local Similarity 100.
Matches 9; Conservative
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Matches 9; Conservative
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ORGANISM: Homo sapiens
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LENGTH: 12
  Query Match
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Sequence 2, Application US/08929095
; GENERAL INFORMATION:
    APPLICANT: Sportsman, Richard
    APPLICANT: Sportsman, Richard
    APPLICANT: Cairns, Nicholas
    APPLICANT: Villar, Hugo
    APPLICANT: Lee, Sandra
    TITLE OF INVENTION: COMPETITIVE BINDING FLUORESCENCE POLARIZATION ASSAY
    FILE REFREENCE: 22560203900
    CURRENT APPLICANT: USBER: US/08/929,095
    CURRENT FILING DATE: 1997-09-15
    NUMBER OF SEQ ID NOS: 4
    SOFTWARE: Patentin Ver. 2.0
    SEQ ID NO 2
    LENGTH: 17
                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Koister, Hubert
APPLICANT: Siddiqi, Suhaib
APPLICANT: Siddiqi, Suhaib
APPLICANT: Siddiqi, Suhaib
APPLICANT: Siddiqi, Suhaib
APPLICANT: Little, Daniel
TITLE OF INVENTION: Capture Compounds, Collections Thereof
TITLE OF INVENTION: Compositions
FILE REFERENCE: 24743-2305
CURRENT APPLICATION NUMBER: PCT/US02/22821
CURRENT FILING DATE: 2002-07-16
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                                                                            Score 53; DB 11; Length 16; Pred. No. 0.49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 53; DB 13; Length 17;
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; OTHER INFORMATION: Pyroglutamic acid residue US-08-798-423-6
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PRIOR APPLICATION NUMBER: 60/306,019

PRIOR FILING DATE: 2001-07-16

PRIOR APPLICATION NUMBER: 60/314,123

PRIOR APPLICATION NUMBER: 60/314,123

PRIOR APPLICATION NUMBER: 60/363,433

PRIOR FILING DATE: 2000-08-21

NUMBER OF SEQ ID NOS: 149

SEQ ID NO 60

LEWRTH: 17
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                                                                                                                                0: Mismatches
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; Sequence 60, Application PC/TUS0222821
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: HK Pharmaceuticals, Inc.
                                                                              100.0%;
100.0%;
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ORGANISM: Artificial Sequence
FEATURE:
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Best Local Similarity 100.
Matches 9; Conservative
                                                                              Query Match 100.

Best Local Similarity 100.

Matches 9; Conservative
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GENERAL INFORMATION:
APPLICANT: Gevas, Philip C.
APPLICANT: Karr, Stephen L.
APPLICANT: Michaell, Dov
FILE REFERENCE: 1102865-0031
CURRENT APPLICATION NUMBER: 06/011,411
PRIOR APPLICATION NUMBER: 06/011,411
PRIOR APPLICATION NUMBER: 06/011,411
SEQ ID NOS: 8
SOFTWARE: PatentIn Ver: 2.1
SEQ ID NO 6
LENGTH: 166
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                                                                                                                   COMPUTER READBLE FORM:

MEDIUM TYPE: Floppydisk
COMPUTER: Lab PC compatible
COMPUTER: Patentin PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRIT APPLICATION DATA:
APPLICATION NUMBER: US/10/016,306
FLING DATE: 10-Dec-2001
CLASSIFICATION: CUNKnown>
PRIOR APPLICATION CUNKnown>
PRIOR APPLICATION NUMBER: US/09/506,854
FILING DATE: 16-DEC-1997
APPLICATION NUMBER: US 08/991,953
FILING DATE: 16-DEC-1997
APPLICATION NUMBER: US 08/652,971
FILING DATE: 24-MAY-1996
ATTORNEY/AGENT NUMBER: US 08/652,971
FILING DATE: 24-MAY-1996
         STREET: 4 Embarcadero Center, Suite 3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Vance, DOLLY A.

REGISTRATION NUMBER: 39,054

REFERENCE/DOCKET NUMBER: 3-63478-4/DAV

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 781-1989

TELERX: (415) 388-3249

INFORMATION FOR SEQ ID NO: 10:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-10-016-306-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
                                CITY: San Francisco
STATE: California
COUNTRY: United Sta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100...
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LOCATION: (1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-798-423-6
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ORGANISM: Homo Sapien
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                                                                                                                                                                                                                                                                                                                  RESULT 15
PCT-US94-04832A-75
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                                                 US-10-197-954-60
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APPLICANT: Bridon, Dominique
APPLICANT: Bridon, Dominique
APPLICANT: Bridon, Dominique
APPLICANT: Bridon, Alan
APPLICANT: Milner, Peter
APPLICANT: Holmes, Darren
TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
TITLE OF INVENTION: COMPONENTS ACTIVITY THROUGH CONJUGATION TO BLOOD
TITLE OF INVENTION: COMPONENTS (05/09/657,276
CURRENT APPLICATION NUMBER: US/09/657,276
PRIOR APPLICATION NUMBER: 60/133,406
PRIOR PLING DATE: 1999-05-17
PRIOR PLING DATE: 1999-010-18
PRIOR FILING DATE: 1999-10-18
SOFTWARE: PALECATION NUMBER: 60/153,406
PRIOR FILING DATE: 1999-10-18
SOFTWARE: PALECATION NUMBER: 60/153,783
PRIOR FILING DATE: 1999-10-18
SOFTWARE: PALECATION NUMBER: 1999-10-18
SOFTWARE: PALECATION NUMBER: 1999-10-18
SOFTWARE: PALECATION NUMBER: 1999-10-18
SOFTWARE: PALECATION NUMBER: 1999-10-18
SEQ ID NO 422
LENGTH: 17
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GENERAL INFORMATION:

APPLICANT: K'ster, Hubert

APPLICANT: Siddiqi, Suhaib

APPLICANT: Little, Daniel

TITLE OF INVENTION: Capture Compounds, Collections Thereof

TITLE OF INVENTION: Compositions

TITLE OF INVENTION: Compositions

FILE REFERENCE: 24743-2305

CURRENT APPLICATION NUMBER: US/10/197,954

CURRENT APPLICATION NUMBER: 60/306,019

PRIOR APPLICATION NUMBER: 60/314,123

PRIOR PELING DATE: 2001-07-16

PRIOR PPLICATION NUMBER: 60/314,123

PRIOR PLING DATE: 2001-03-11

NUMBER OF SEQ ID NOS: 149

SOFTWARE: FastSEQ for Windows Version 4.0

LENGTH: 17
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                        0; Indels
  Pred. No. 0.52;
                        Mismatches
                                                                                                                                                                                                                                       Sequence 422, Application US/09657276
GENERAL INFORMATION:
APPLICANT: Conjuchem, Inc.
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100.08;
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Best Local Similarity 100.
Matches 9; Conservative
Best Local Similarity 100.
Matches 9; Conservative
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APPLICANT: Ladd, Anna
APPLICANT: Ladd, Anna
APPLICANT: Ladd, Chang Yi
APPLICANT: Camb, Timothy
TITLE OF INVENTION: Immunogenic LHRH peptide constructs
TITLE OF INVENTION: and synthetic universal immune stimulators for vaccines
NUMBER OF SEQUENCES: 114
CORRESPONDENCE ADDRESS:
ADDRESSEE:
STREET: 400 Garden City Plaza
CITY: Garden City
CITY: Garden City
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COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/04832A
FILING DATE: 13-APR-1994
100.0%; Score 53; DB 25;
100.0%; Pred. No. 0.52;
live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 50; DB
Pred. No. 1.1;
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                                                                                                                                                                                                           Sequence 75, Application PC/TUS9404832A GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER:
TELECOMUNICATION INFORMATION:
TELEPHONE: (516)742-4343
TELEFAX: (516)742-4366
INFORMATION FOR SEQ ID NO: 75:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       94.3%;
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CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 88.2
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 Query Match 100.
Best Local Similarity 100.
Matches 9; Conservative
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PCT-US94-04832A-75
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Sequence 140, Application US/10302267
GENERAL INFORMATION:
APPLICANT: Keddie, James
APPLICANT: Fromm, Michael
APPLICANT: Heard, Jacqueline
APPLICANT: Riechmann, Jose Luis
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Broun, Pierre
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US-10-302-267-140
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APPLICANT:
APPLICANT:
APPLICANT:
SEQ ID NO 7
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Sequence 138, App
Sequence 114, App
Sequence 114, App
Sequence 1980, App
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Sequence 138, 7
Sequence 114, 7
                                                                                                            2003, 09:48:01; Search time 14.5714 Seconds (without alignments) 50.530 Million cell updates/sec
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2: /cgn2_6/ptodata/1/paa/USO6_NEW_COMB.pep:*

3: /cgn2_6/ptodata/1/paa/USO8_NEW_COMB.pep:*

4: /cgn2_6/ptodata/1/paa/USO8_NEW_COMB.pep:*

5: /cgn2_6/ptodata/1/paa/USO_NEW_COMB.pep:*

5: /cgn2_6/ptodata/1/paa/USO8_NEW_COMB.pep:*

7: /cgn2_6/ptodata/1/paa/USO8_NEW_COMB.pep:*

7: /cgn2_6/ptodata/1/paa/USO8_NEW_COMB.pep:*
               GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-10-278-138-138
US-10-278-536-114
US-10-278-536A-114
US-10-218-140-1980
US-10-218-140-1980
US-10-218-140-1980
US-10-218-140-1980
US-10-288-798-24
US-10-724-676-86993
US-10-278-536-206
US-10-278-536-206
US-09-724-676-86996
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| S-09-724-676A-56304
| S-09-724-676-56305
| S-09-724-676-56305
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-09-724-676A-86995
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US-09-724-676-51590
US-09-724-676-51591
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Maximum Match 1008
Listing first 45 summaries
                                                                                protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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length: 2000000000
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53
1 EGPWLRERF 0
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Match Length DB
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Sequence 7, Application US/10314057

GENERAL INFORMATION:

APPLICANT: Geves, Philip

APPLICANT: Stephen, Grimes

APPLICANT: Rarr, Stephen

APPLICANT: Michaeli, Dov

TITLE OF INVENTION: Method for the Treatment of Gastroesophageal Reflux Disease

FILE REFERENCE: ACGIUSA

CURRENT APPLICATION NUMBER: US/09/700,378

PRIOR FILING DATE: 12000-11-14

PRIOR APPLICATION NUMBER: US/09/10734

PRIOR PILING DATE: 1999-05-14

PRIOR PILING DATE: 1999-05-14

PRIOR APPLICATION NUMBER: 60/085,610

PRIOR FILING DATE: 1998-05-15

NUMBER OF SEO ID NOS: 8

SOFTWARE: PatentIn version 3.0
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                     US-09-724-676-51593
US-09-724-676-51594
US-09-724-676-51596
US-09-724-676-51596
US-09-724-676-51598
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100.0%; Pred. No. 3.4e+05;
ive 0; Mismatches 0;
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Best Local Similarity 100.
Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Broun, Pierre
TITLE OF INVENTION: STRESS-INDUCED POLYNUCLEOTIDES
FILE REFERENCE: MBI-011
CURRENT APPLICATION NUMBER: US/10/278,536
CURRENT FILING DATE: 2002-10-22
PRIOR FILING DATE: 1999-03-23
NUMBER OF SEQ ID NOS: 238
SOFTWARE: Patentin Ver: 2.1
SEQ ID NO 114
LENGTH: 349
                                                                                                                                                                                                  core 40; DB 6;
red. No. 38;
Mismatches 1
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Pred. No. 3
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 114, Application US/10278536 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Reuber, Lynne
Riechmann, Jose-Luis
Yu, Guo-Liang
Keddie, James
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Riechmann, Jose-Luis
                                                                                      TYPE: PRT
ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                  75.5%;
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PRIOR FILING DATE: 1999-03-23
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APPLICANT: Heard, Jacqueline
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Yu, Guo-Liang
Keddie, James
Ratcliffe, Oliver
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Jiang, Cai-Zhong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Jiang, Cai-zhong
Pineda, Omaira
Reuber, Lynne
                NUMBER OF SEQ ID NOS: 177
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                               Query Match
Best Local Similarity 66./.
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Adam, Luc
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Best Local Similarity 66.7
Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Samaha, Raymond
                                                                                                                        ; FEATURE:
; OTHER INFORMATION: G220
US-10-278-173-138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: G220
US-10-278-536-114
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15 KGPWLPEED 23
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15 KGPWLPEED 23
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                              SOFTWARE: Pate
SEQ ID NO 138
LENGTH: 349
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APPLICANT:
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TITLE OF INVENTION: POLYNUCLEOTIDES FOR ROOT TRAIT ALTERATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 6; Length 238;
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Pred. No. 4;
1; Mismatches
                                                                                                                                     TITLE OF INVENTION: PLANT GENE SEQUENCES II FILE REFERENCE: MBI-0007 CURRENT APPLICATION NUMBER: US/10/302,267 CURRENT FILING DATE: 2002-11-22
                                                                                                                                                                                        CURREWY FILING DATE: 2002-11-22
PRIOR APPLICATION NUMBER: US/09/506,720
PRIOR PELING DATE: 2000-02-17
PRIOR PELING DATE: 1099-02-18
PRIOR PELICATION NUMBER: 60/120,880
PRIOR PELICATION NUMBER: 60/121,037
PRIOR FILING DATE: 1999-02-22
PRIOR PELICATION NUMBER: 60/124,278
PRIOR PELICATION NUMBER: 60/129,450
PRIOR APPLICATION NUMBER: 60/129,450
PRIOR PELICATION NUMBER: 60/129,450
PRIOR PELICATION NUMBER: 60/144,153
PRIOR PELICATION NUMBER: 60/161,143
PRIOR FILING DATE: 1999-07-15
PRIOR PELICATION NUMBER: 60/161,143
PRIOR FILING DATE: 1999-07-15
PRIOR FILING DATE: 1999-10-22
PRIOR FILING DATE: 1999-10-22
PRIOR FILING DATE: 1999-10-22
PRIOR FILING DATE: 1999-10-22
PRIOR FILING DATE: 1999-11-01
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CURRENT APPLICATION NUMBER: US/10/278,173
CURRENT FILING DATE: 2002-10-21
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PRIOR FILING DATE: 2000-03-22
PRIOR APPLICATION NUMBER: 60/125,814
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APPLICANT: Broun, Pierre
APPLICANT: Riechmann, Jose-Luis
APPLICANT: Pineda, Omaira
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           84.9%;
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Ratcliffe, Oliver
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Pilgrim, Marsha
Keddie, James
                                                Yu, Guo-Liang
Jiang, Cai-Zhong
                                                                                                                        Creelman, Robert
                                                                                                       Pilgrim, Marsha
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Best Local Similarity 87.5
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: G1311
US-10-302-267-140
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                                                                                    Samaha,
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APPLICANT: Gevas, Philip
APPLICANT: Stephen
APPLICANT: Stephen
APPLICANT: Stephen
APPLICANT: Stephen
APPLICANT: Stephen
APPLICANT: Machaeli, Dov
TITLE OF INVENTION: Method for the Treatment of Gastroesophageal Reflux Disease
FILE REFERENCE: ACGIUGA
CURRENT APPLICATION NUMBER: US/10/314,057
FRIOR PELING DATE: 2000-11-14
PRIOR APPLICATION NUMBER: PCT/US99/10734
PRIOR FILING DATE: 1999-05-14
PRIOR APPLICATION NUMBER: 60/085,610
PRIOR FILING DATE: 1998-05-15
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIn version 3.0
SEQ ID NO 1
LENGTH: 12
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                                                                Catherine M.;
                                                BAUGHN, Mariah R.; TRIBOULEY, Catherine M.;
THORNTON, Michael; ELLIOTT, Vicki S.;
LU, Yan; ISON, Craig H.;
AU-YOUNG, Janice; TANG, Y. Tom;
AZIMZAI, Yalda; BURRILL, John D.;
MARCUS, Gregory A.; ZINGLER, Kurt A.;
LU, Dyung Aina M.; LAL, Preeti G.;
KRAMKUMAR, Jayalaxmi; WARREN, Bridget A.;
KEARNEY, Liam; POLLCKY, Jennifer L.;
THANGAVELU, Kavitha; BURFORD, Neil
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Pred. No. 2e+02;
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US-10-288-798-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT FILING DATE: 2002-11-01
PRIOR APPLICATION NUMBER: 9C7/US01/27219
PRIOR FILING DATE: 2001-08-31
PRIOR FILING DATE: 2001-08-31
PRIOR PILING DATE: 2001-01-3
PRIOR FILING DATE: 2000-10-13
PRIOR FILING DATE: 2000-10-13
PRIOR PLICATION NUMBER: US 60/236,499
PRIOR PLICATION NUMBER: US 60/236,499
PRIOR PLICATION NUMBER: US 60/234,902
PRIOR APPLICATION NUMBER: US 60/234,902
PRIOR PLING DATE: 2000-09-29
PRIOR PLING DATE: 2000-09-14
PRIOR FILING DATE: 2000-09-14
PRIOR FILING DATE: 2000-09-14
PRIOR FILING DATE: 2000-09-08
PRIOR PLILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
PRIOR PLILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
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FILE REFERENCE: PI-0209 USA
CURRENT APPLICATION NUMBER: US/10/288,798
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85.7%;
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Best Local Similarity 85...
6, Conservative
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APPLICANT:
APPLICANT:
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APPLICANT: Leach, Martin D.
APPLICANT: Shimkets, Richard A.
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES AND POLYPEPTIDES
TITLE OF INVENTION: ENCODED THEREBY
FILE REFERENCE: 15966-543 CON
CURRENT APPLICATION NUMBER: US/10/218,140
CURRENT APPLICATION NUMBER: 09/540,763
PRIOR PILING DATE: 2000-03-30
PRIOR PILING DATE: 1999-04-05
PRIOR PELICATION NUMBER: 60/127,636
PRIOR PELICATION NUMBER: 60/127,636
PRIOR PELICATION NUMBER: 60/127,636
PRIOR PELICATION NUMBER: 60/127,636
PRIOR PELICATION NUMBER: 60/127,637
PRIOR PELICATION NUMBER: 60/127,637
PRIOR PELICATION NUMBER: 60/127,637
PRIOR APPLICATION NUMBER: 60/127,637
PRIOR PELICATION NUMBER: 60/127,637
PRIOR PELICATION NUMBER: 60/127,637
PRIOR PELICATION NUMBER: 60/127,637
PRIOR PELICATION NUMBER: 60/127,607
PRIOR APPLICATION NUMBER: 60/127,607
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                                                    APPLICANT: APELCANT: APELCANT: APPLICANT: Broun, Pierre
APPLICANT: Broun, Pierre
TITLE OF INVENTION: STRESS-INDUCED POLYNUCLEOTIDES
FILE REFERENCE: MBI-011
CURRENT APPLICATION NUMBER: US/10/278,536A
CURRENT FILING DATE: 2002-12-09
PRIOR APPLICATION NUMBER: 60/125,814
PRIOR PILING DATE: 1999-03-23
NUMBER OF SEQ ID NOS: 238
SOFTWARE: Patentin Ver: 2.1
SEQ ID NO 114
LENGTH: APPLICATION OF 124
LENGTH
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; Sequence 24, Application US/10288798
; GENERAL IRFORMATION:
; APPLICANT: BANDMAN, Olga: NGUYEN, Danniel B;
; APPLICANT: WALIA, Narinder K.; HARALIA, April J.A.;
; APPLICANT: YAO, Monique G.; GANDHI, Ameena R.;
; APPLICANT: GURURAJAN, Rajagopal; DING, Li;
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Pred. No. 38;
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Pred. No. 1.4e+02
1; Mismatches
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ORGANISM: Arabidopsis thaliana
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75.0%;
Ratcliffe, Oliver
                                        Pilgrim, Marsha
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Best Local Similarity 66.7
Matches 6; Conservative
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; OTHER INFORMATION: G220
US-10-278-536A-114
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; ORGANISM: Homo sapiens
US-10-218-140-1980
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Best Local Similarity
Matches 6; Conserv
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15 KGPWLPEED 23
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171 @PWAEEEK 178
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US-10-218-140-1980
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LENGTH: 929
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Pred. No. 62;
3; Mismatches 1; Indels
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Pred. No. 62;
                                                                                                                                DB 6; Length 12; 3.6;
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GENERAL INFORMATION:

APPLICANT: Compugen LTD

TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen

CURRENT APPLICATION NUMBER: US/09/724,676A

CURRENT FILING DATE: 2000-11-28

NUMBER OF SEQ ID NOS: 97222

SOFTWARE: Patentin version 3.2

LENGTH: 173
                                                                                                                                                                                                                                                                                                           Sequence 86993, Application US/09724676
GENERAL INFORMATION:
APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: Patentin version 3.2
ENGTH: 173
                                                                                                                                  71.7%; Score 38; DB 100.0%; Pred. No. 3.6 iive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3; Mismatches
                                                 NAME/KEY: MOD_RES
: LOCATION: (1)...(1)
: COCATION: (1)...(1)
: OTHER INFORMATION: pyroglutamic acid
US-10-314-057-1
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US-10-278-536-206
Sequence 206, Application US/10278536
; GENERAL INFORMATION:
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55.6%;
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55.6%;
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Best Local Similarity 55.6
Matches 5; Conservative
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Best Local Similarity 100.
Matches 6; Conservative
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Best Local Similarity 55.6
Matches 5; Conservative
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US-09-724-676A-86993
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CORGANISM: Homo sapiens
US-09-724-676-86993
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US-09-724-676A-86993
   TYPE: PRT
ORGANISM: human
FEATURE:
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55.6%; Pred. No. 1.2e+02;
tive 3; Mismatches 1; Indels
                                                                                                                                                                                                         TITLE OF INVENTION. PIERTE
TITLE OF INVENTION. STRESS-INDUCED POLYNUCLEOTIDES
FILE REPERENCE: MBI-011
CURRENT APPLICATION NUMBER: US/10/278,536
CURRENT FILING DATE: 2002-10-22
PRIOR APPLICATION NUMBER: G0/125,814
PRIOR PLING DATE: 1999-03-23
NUMBER OF SEQ ID NOS: 238
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 206
LENGTH: 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Adam, Luc
APPLICANT: Broun, Pierre
FITLE OF INVENTION: STRESS-INDUCED POLYNUCLEOTIDES
FILE REFERENCE: MBI-011
CURRENT APPLICATION NUMBER: 105/10/278,536A
CURRENT FILING DATE: 2002-12-09
PRIOR FILING DATE: 1999-03-23
NUMBER OF SEQ ID NOS: 238
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 206, Application US/10278536A GENERAL INFORMATION:
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Yu, Guo-Liang
Keddie, James
Ratcliffe, Oliver
Pilgrim, Marsha
Adam, Luc
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Keddie, James
Ratcliffe, Oliver
Pilgrim, Marsha
Adam, Luc
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55.6%;
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APPLICANT: Heard, Jacqueline
APPLICANT: Jiang, Cai-Zhong
APPLICANT: Pineda, Omaira
APPLICANT: Reuber, Lynne
Heard, Jacqueline
Jiang, Cai-Zhong
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Best Local Similarity 55.6
Matches 5; Conservative
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Best Local Similarity 55.6
Matches 5; Conservative
                                         Pineda, Omaira
Reuber, Lynne
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; OTHER INFORMATION: G216
US-10-278-536-206
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US-10-278-536A-206
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50 KGPWLPEQD 58
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Best Local Similarity 55.6%; Pred. No. 1.6e+02;
Matches 5; Conservative 3; Mismatches 1; Indels
                                                                                                                            Sequence 86996, Application US/09724676
GENERAL INFORMATION:
APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676
CURRENT FILING DATE: 2000,11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: Patentin version(3.2)
LENGTH: 493
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0.85.09-724-676A-86996
Sequence 86996, Application US/09724676A
GENERAL INFORMATION:
APPLICANT: Compugen LTD:
TTTLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676A
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: Patentin version 3.2
SEQ ID NO 86996
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GENERAL INFORMATION:
APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676
CURRENT FILIG DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SEQ ID NO 86994
LENGTH: 538
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CORGANISM: Homo sapiens
US-09-724-676-86996
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; ORGANISM: Homo sapiens
US-09-724-676A-86996
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US-09-724-676-86994
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87 KGPWTKEED 95
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87 KGPWTKEED 95
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US-09-724-676-86996
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US-09-724-676-86994
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      Query Match
      69.8%; Score 37; DB 5; Length 538;

      Best Local Similarity 55.6%; Pred. No. 1.8e+02;

      Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

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      Search completed: February 5, 2003, 09:50:58

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Human gastrin G34
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Novel human secret
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Human polypeptide
Human polypeptide
Antigenic peptide
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                                                                                                                        5, 2003, 09:40:45; Search time 35.4286 Seconds (without alignments) 45.133 Million cell updates/sec
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/SIDS2/ggdate/geneseq/geneseqp-emb1/AA1993.DAT;*
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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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Listing first 45 summaries
                                                                               OM protein - protein search, using sw model
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## ALIGNMENTS

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Antigenic peptide fragment selected from the 22 N-terminal AAs of tetrateseracontagastrin (G34).
                                                                                                       Gastrin; tumours; peptic ulcers; diptheria toxoid; tetanus toxin;
                                                                                                                                                                                                                                                                            Immunogens against gastrin peptide(s) - used to induce antibodies that specifically neutralise single form of gastrin, G17 or G34
                                                                                                                                                                                                                                         Littenberg RL;
                AAR06335 standard; protein; 12 AA
                                                                                                                                                                                                                                       Karr SL,
                                                                                                                                                                   90EP-0300456
                                                                                                                                                                                      89US-0351193
89US-0301353
                                                         (first entry)
                                                                                                                                                                                                                                      Gevas PC, Grimes S,
                                                                                                                                                                                                                   (APHT-) APHTON CORP.
                                                                                                                                                                                                                                                          WPI; 1990-233029/31.
                                                                                                                                                                   17-JAN-1990;
                                                                                                                                                                                     12-MAY-1989;
24-JAN-1989;
                                                         07-DEC-1990
                                                                                                                                               01-AUG-1990
                                                                                                                           EP380230-A.
                                     AAR06335;
RESULT 1
         AAR06335
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Claim 12; Page 19; 32pp; English

AAY49307 AAR62738 AAU30337 AAU30339 AAO07572 AAO00748

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Human gastrin G34 derived immunogen hG34(6).
              AAY51313 standard; peptide; 12 AA
                                                                          (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 ELGPQGRPPPPC 12
                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2000-116301/10.
                                                                                                                                                                                                                                                                                                                                        (APHT-) APHTON CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
Matches 12; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                           15-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      06-MAR-2000
                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                               W09959631-A1
                                                                                                                                                                                                                                                                             14-MAY-1999;
                                                                          14-APR-2000
                                                                                                                                                                                                                                             25-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic
                                                                                                                                                                                                                                                                                                                                                                      Gevas PC,
                                                                                                                                                                                                                                                                                                                                                                                                                                 Treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY49307
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                                            ōλ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0
                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                  Immunogenic; treatment; hypergastrinemia; gastrin G17; gastrin G34;
pernicious anemia; anti-ulceq; proton pump inhibitor; colorectal disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This invention describes a novel method for the treatment or preventing hypergastrinemia by administering to a patient a gastrin G17 and/or G34 peptide fragment linked by an amino acid spacer to an immunogenic carrier. The methods are used to treat hypergastrinemic patients, particularly those with pernicious anemia, those receiving treatment with anti-ulcer agents such as proton pump inhibitors (particularly momeprazole or lansoprazole) or H.2 receptor blocking agents or antagonists, or those having colorectal disorders or diseases. This sequence represents the human gastrin G34 peptide which is used to illustrate the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    reating or preventing hypergastrinemia comprising administration of,
                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
0
                                                                                                                                        0
Antigenic fragments may be attached to an immunogenic carrier and used to raise Abs to a specific single form of Gastrin ie. G17 or G34. Peptide fragments capable of binding to these Abs are useful in neutralising anti-gastrin Abs in vivo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 75; DB 21; Length 12; Llarity 100.0%; Pred. No. 0.00093; Conservative 0; Mismatches 0; Indels
                                                                                                         ; Score 75; DB 11; Length 12;
; Pred. No. 0.00093;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ŝ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Watson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Michaeli D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 11; 44pp; English.
                                                                                                                                                                                                                                                                             AAY51306 standard; peptide; 12 AA.
                                                                                                          100.0%;
100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99WO-US10751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98US-0085714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Karr
                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                      Human gastrin G34 peptide
                                                                                                          Query Match 100.
Best Local Similarity 100.
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ELGPQGRPPPPC 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 ELGPQGRPPPPC 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Grimes S,
                                                                                                                                                                     1 ELGPQGRPPPPC 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (APHT-) APHTON CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2000-116301/10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
nes 12; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12 AA;
                                                                            12 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             W09959631-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-MAY-1998;
                                                                                                                                                                                                                                                                                                                                         14-APR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gevas PC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                               Seguence
                                                                                                                                                                                                                                                                                                           AAY51306;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Loca
Matches
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                                                                                                                                                                                                                                                  RESULT 2
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RESULT 3

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Immunogenic; treatment; hypergastrinemia; gastrin G17; gastrin G34;
pernicious anemia; anti-ulcer; proton pump inhibitor; colorectal disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This invention describes a novel method for the treatment or preventing hypergastrinemia by administering to a patient a gastrin G17 and/or G34 peptide fragment linked by an amino acid spacer to an immunogenic carrier. The methods are used to treat hypergastrinemic patients, particularly those with pernicious anemia, those receiving treatment with anti-ulcer agents such as proton pump inhibitors (particularly comeprazole or lansoprazole) or H.2 receptor blocking agents or antagonists, or those having colorectal disorders or diseases. This sequence represents a human gastrin G34 derived immunogen which is used to illustrate the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gastroesophageal reflux disease; GERD; gastrin; anti-gastrin antibody; histamine H_2; proton pump inhibitor; acid output; stomach; therapy; esophagitis; immunogen; human; tetratriacontagastrin; G34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     or preventing hypergastrinemia comprising administration of,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human tetratriacontagastrin (G34) immunogenic peptide 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 75; DB 21; 100.0%; Pred. No. 0.00093;
                                                                                                                                                                                                                                                                                                                                                                                                                           Michaeli D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 3; Page 18; 44pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY49307 standard; peptide; 12 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                              Karr S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     e.g. anti-gastrin antibodies
                                                                                                                                                                                                                                                         99WO-US10751.
                                                                                                                                                                                                                                                                                                              98US-0085714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Key
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Ladd AE, Wang CY,
                                                                                                    WPI; 1994-357910/44.
                                                                                                                                                                                                                                                                                                                                                                                                        1 ELGPQGRPPPP 11
                                                                                                                                                                                                                                                                                                                                                                                                                  (HYSE-) HYSEQ INC
                                         .
К
                                                                                                                                                                                                                                                                                                                                           11 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tang YT, Liu C,
                                         AUF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200179449-A2.
                                       (LADD/) LADD A (WANG/) WANG C (ZAMB/) ZAMB T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
          27-APR-1993;
                     14-APR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25-OCT-2001.
                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAU30337;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 6
AAU30337
   δλ
                                                                                                                                                                                                                                                                                                                                                                                                                           Dp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        disease (GERD) that comprises administering to a patient an immunogenic composition which generates anti-gastrin antibodies, which bind to gastrin, in a patient; and administering histamine H_2 antagonist or a proton pump inhibitor. The method provides a more effective method for controlling acid output by the stomach. The therapy is less costly. High gastrin levels associated with standard therapies are neutralized and undesirable side effects are reduced. The method permits a reduced closate of acid reducing agent both at the acid producing level as well as the acid production stimulating level (gastrin). Reduction of dosages is desirable for prolonged treatment of GERD. In a combination therapy with H_2 agonists or proton pump inhibitors, anti-gastrin 17 antibody titers can be maintained by occasional booster shots while gastric acid inhibitor dosing is reduced. Immunization allows a sufficient time for the esophagitis to completely heal and no surgery is required. The munogenic peptide.

ANY49307-308 represent human tetratriacontagastrin (G34)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Helper T cell epitope; universal immune stimulator; invasin; hapten; gastrin; peptic ulcers; gastrin-stimulated tumours.
                                                                                                                                                                                                                          invention relates to the treatment of gastroesophageal reflux
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
                                                                                                                                                                                  Method for treatment of gastroesophageal reflux disease (GERD)
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score.75; DB 21;
ilarity 100.0%; Pred. No. 0.00093;
Conservative 0; Mismatches 0;
                                                                                                                                           Michaeli D;
         /label= pglu
/note= "pyroglutamate"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAR62738 standard; peptide; 11 AA.
                                                                                                                                                                                                     Example 4; Page 11; 24pp; English.
                                                                                                                                           Karr S,
                                                                                                  98US-0085610.
                                                                                99WO-US10734.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                           Grimes S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 ELGPQGRPPPPC 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 ELGPQGRPPPPC 12
                                                                                                                       (APHT-) APHTON CORP.
                                                                                                                                                             WPI; 2000-062378/05.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                     12 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gastrin hapten.
Modified-site
                                                                                                  L5-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-SEP-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28-APR-1994;
                                                                               14-MAY-1999;
                                       WO9959612-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO9425060-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10-NOV-1994
                                                           25-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12;
                                                                                                                                         Gevas PC,
                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAR62738;
                                                                                                                                                                                                                                                                                                                                                                                                                peptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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synthetic immunogenic peptides are provided in which a universal immune stimulator is linked to a peptide or protein hapten containing B cell and/or cytotoxic T lymphocyte epitopes, giving a product which causes potent immune responses to the coupled peptide or protein. The stimulator consists of (A) a promiseous helper T cell epitope (Th) which elicits an immune response to the coupled peptide in members of a heterogeneous population expressing diverse HLA phenotypes, and (B) an adjuvant peptide sequence from the invasin protein of Yersinia. Spacer amino acid sequences (e.g. Gly-Gly) can be provided between the invasin and Th domains and between the immune stimulator and hapten components. When the hapten is LHRH, then optionally the invasin domain can be omitted from the immune stimulator component.

The present sequence is an example of a gastrin hapten which can be benefit of the immune stimulator to form a vaccine for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human, vaccination; gene therapy; nutritional supplement;
stem cell proliferation; haematopoiesis; nerve tissue regeneration;
immune suppression; immune stimulation; anti-inflammatory; leukaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
0
                                                                                                                                                                                                                                                                                                                                                                                                Immunogenic luteinising hormone releasing hormone peptide(s) that suppress LHRH activity in males and females
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 56; DB 15; Length 11;
Pred. No. 0.29;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     peptic ulcer disease or gastrin-stimulated tumours
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claims 27, 37; Page 96; 213pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAU30337 standard; Protein; 139 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel human secreted protein #828.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   74.7%;
81.8%;
93US-0057166.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-APR-2001; 2001WO-US08656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18-APR-2000; 2000US-0552929
26-JAN-2001; 2001US-0770160
                                                                                                                                                                                                                                                  Zamb T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
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06-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      disorders
                                                                                                                                                                                                                                                               Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAO07572;
                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                AAO07572
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                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                    polypeptides and antibodies to the polypeptides are useful for determining the presence of or predisposition to a disease associated with altered levels of polypeptide. The polypeptides are also useful for identifying agents (agonists and antagonists) that bind to them. Cells expressing the proteins are useful for identifying a therapeutic agent for use in treatment of a pathology related to aberrant expression or physiological interactions of the polypeptide. Vectors comprising the nucleic acids encoding the polypeptides and cells genetically engineered to express them are also useful for producing the proteins. The proteins are useful in genetic vaccination, testing and threapy, and can be useful the pulphalments. They may be used to increase stem cell proliferation; to regulate haematopoiesis; and in bone, cartilage, tendon and/or nerve tissue growth or regeneration;
                                                                                                                                                                                                                                                                                                                          and
                            Nucleic acids encoding a range of human polypeptides, useful in genetic vaccination, testing and therapy ^{\circ}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nucleic acids encoding a range of human polypeptides, useful in genetic
                                                                                                                                                                                                                                                                                                       bone, cartilage, tendon and/or nerve tíssue growth or regeneration;
immune suppression and/or stimulation; as anti-inflammatory agents; and
in treatment of leukaemias. AAU29510-AAU33304 represent the amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; vaccination; gene therapy; nutritional supplement; stem cell proliferation; haematopoiesis; nerve tissue regeneration; immune suppression; immune stimulation; anti-inflammatory; leukaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                .
0
                                                                                                          secreted polypeptides.
                                                                                                                                                                                                                                                                                                                                                     sequences of novel human secreted proteins of the invention
                                                                                                                                                                                                                                                                                                                                                                                                              Length 139;
                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                Score 55; DB 22;
Pred. No. 3.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                             2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 20; Page 279-280; 765pp; English
                                                                                                          invention relates to novel human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAU30339 standard; Protein; 169 AA.
                                                                          Claim 20; Page 279; 765pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel human secreted protein #830.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               vaccination, testing and therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tang YT, Liu C, Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                             73.3%;
72.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16-APR-2001; 2001WO-US08656
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26-JAN-2001; 2001US-0770160
                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Query Match
Best Local Similarity 72./*,
Best Local Similarity 72./*,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
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WPI; 2001-611725/70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 ELGPQGRPPPP 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29 QISPQGRPPPP 39
                                                                                                                                                                                                                                                                                                                                                                                  139 AA;
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                                                                                                                                                                                                                                                                                                                                                                                     Sequence
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The invention relates to novel human secreted polypeptides.

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polypeptides and antibodies to the polypeptides are useful for determining the presence of or predisposition to a disease associated with altered levels of polypeptide. The polypeptides are also useful for identifying agents (agonists and antaqonists) that bind to them. Cells expressing the proteins are useful for identifying a therapeutic agent for use in treatment of a pathology related to aberrant expression or physiological interactions of the polypeptide. Vectors comprising the nucleic acids encoding the polypeptides and cells genetically engineered to express them are also useful for producing the proteins. The proteins are useful in genetic vaccination, testing and therapy, and can be used as untritional supplements. They may be used to increase stem cell proliferation; to regulate haematopoiesis; and in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorders; arthritis; inflammation.
                                                                                                                                                                                                                                                                                        bone, cartilage, tendon and/or nerve tissue growth or regeneration; immune suppression and/or stimulation; as anti-inflammatory agents; and in treatment of leukaemias. AAU39510-AAU33304 represent the amino acid sequences of novel human secreted proteins of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to human polynucleotides (AAI79941-AAI93841) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukaemia, inflammation and immune discorders
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 22; Length 169;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. 4.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AA007572 standard; Protein; 112 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human polypeptide SEQ ID NO 21464.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         73.38;
72.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pang YT, Liu C, Drmanac RT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28-FEB-2000; 2000US-0515126.
18-MAY-2000; 2000US-0577409.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                               169 AA;
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AAY51310 standard; peptide; 11
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                                                                                                                                                                                                                                                   (first entry)
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                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (APHT-) APHTON CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Grimes S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1990-233029/31
                                                       Local Similarity
hes 7; Conserv
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les 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 GPQGRPPPPC 12
                  129 AA;
                                                                                                3 GPQGRPPPP 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AA;
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20 GPKGKPPPP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                        AAR06247;
                   Sequence
                                             Query Match
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                                                                       Matches
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                                                                 Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                           Human; cytokine; cell proliferation; cell differentiation; gene therapy; vacchie; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorders; arthritis; inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
e.g. stem cell growth factor activity, haematopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activity/inhibin activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation.
                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukaemia, inflammation and immune
                                                                                                                                                                               ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 20; SEQ ID NO 14640; 1399pp + Sequence Listing; English.
                                                                                                                                                    Length 112;
                                                                                                                                                                             1; Indels
                                                                                                                                                    22;
                                                                                                                                              DB 7
                                                                                                                                                                               Mismatches
                                                                                                                                                  Score 50;
Pred. No.
                                                                                                                                                                                                                                                                                                  AAO00748 standard; Protein; 129 AA.
                                                                                                                                                                                                                                                                                                                                                                                   Human polypeptide SEQ ID NO 14640.
                                                                                                                                              66.7%;
88.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pang YT, Liu C, Drmanac RT;
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18-MAY-2000; 2000US-0577409.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26-FEB-2001; 2001WO-US04927
                                                                                                                                                                                                                                                                                                                                                      06-NOV-2001 (first entry)
                                                                                                                                                                          8; Conservative
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                                                                                                                                                               Best Local Similarity
                                                                                                                      112 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (HYSE-) HYSEQ INC.
                                                                                                                                                                                                       3 GPQGRPPPP 11
                                                                                                                                                                                                                                49 GPOGGPPPP 57
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   07-SEP-2001.
                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                             AAO00748;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        disorders
                                                                                                                                                 Query Match
                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                        RESULT 9
AAO00748
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                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Immunogens against gastrin peptide(s) - used to induce antibodies that specifically neutralise single form of gastrin, G17 or G34 \,
                                                                                                                                                                                                                                                                                                                                                                                                                                      Gastrin; tumours; peptic ulcers; diptheria toxoid; tetanus toxin;
                                                                                                                                                                                                                                                                                                                                                                  Antigenic peptide fragment selected from the 12 N-terminal AAs heptadecagastrin (G17).
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  Length 129,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             65.3%; Score 49; DB 11; Length 11; 80.0%; Pred. No. 2.5;
                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2; Indels
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  22;
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Score 50; DB 2
Pred. No. 17;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human gastrin G17 derived immunogen hG17(5).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
66.7%; Score 50; 77.8%; Pred. No.
                                                                                                                                                                                                                                       AAR06247 standard; protein; 11 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 8; Page 19; 32pp; English.
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N-PSDB; AAI80461
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                              8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 07-SEP-2001
                          Sevas PC,
                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                               AAO00530;
                                                                                                                                                                                                                                         peptides
                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                            RESULT 13
ÖΫ
                                                                                                                                                                                                                                                                                                                              Db
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                                                                                                                                                                                            This invention describes a novel method for the treatment or preventing hypergastrinemia by administering to a patient a gastrin G17 and/or G34 peptide fragment linked by an amino acid spacer to an immunogenic cariter. The methods are used to treat hypergastrinemic patients, particularly those with pernicious anemia, those receiving treatment with anti-ulcer agents such as proton pump inhibitors (particularly omeprazole or lansoprazole) or H_2 receptor blocking agents or antagonists, or those having colorectal disorders or diseases. This sequence represents a human gastrin G17 derived immunogen which is used to illustrate the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gastroesophageal reflux disease; GERD; gastrin; anti-gastrin antibody; histamine H_2; proton pump inhibitor; acid output; stomach; therapy; esophagitis; immunogen; human; heptadecagastrin; G17.
                                                                                                                                                   Treating or preventing hypergastrinemia comprising administration of, e.g. antl-gastrin antibodies
                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                  ;
0
                                                                                                                                                                                                                                                                                                                65.3%; Score 49; DB 21; Length 11; 80.0%; Pred. No. 2.5;
                                                                                                                                                                                                                                                                                                                                  Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human heptadecagastrin (G17) immunogenic peptide 2.
                                                                                                                  Watson
                                                                                                                                                                                                                                                                                                                                  5,
                                                                                                                  Michaeli D,
                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  _label= pGlu
/note= "pyroglutamate"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                 AAY49304 standard; peptide; 11 AA.
                                                                                                                                                                            Example 3; Page 18; 44pp; English.
                                                                                                                  Karr S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99WO-US10734.
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                                                            99WO-US10751
                                                                              98US-0085714
                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                  8; Conservative
                                                                                                                  Grimes S,
                                                                                                (APHT-) APHTON CORP.
                                                                                                                                 WPI; 2000-116301/10
                                                                                                                                                                                                                                                                                                                         Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                    3 GPQGRPPPPC 12
                                                                                                                                                                                                                                                                                                                                                                    2 GPWLRPPPPC 11
                                                                                                                                                                                                                                                                                              11 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Key
Modified-site
         Homo sapiens
                          W09959631-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
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                                                            14-MAY-1999;
                                                                              15-MAY-1998;
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                                           25-NOV-1999
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                                                                                                                  Gevas PC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY49304;
                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                Query Match
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AAY49304
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The invention relates to the treatment of gastroesophageal reflux disease (GERD) that comprises administering to a patient an immunogenic composition which generates anti-gastrin antibodies, which bind to gastrin, in a patient; and administering histamine H.2 antagonist or a proton pump inhibitor. The method provides a more effective method for controlling acid output by the stomach. The therapy is less costly. High gastrin levels associated with standard therapies are neutralized and undesirable side effects are reduced. The method permits a reduced dosage of acid reducing agent both at the acid producing level as well as the acid production stimulating level (gastrin). Reduction of Gosages is desirable for prolonged treatment of GERD. In a combination therapy with H.2 agonists or proton pump inhibitors, anti-gastrin 17 antibody titers can be maintained by occasional booster shots while gastric acid inhibitor dosing is reduced. Immunization allows a sufficient time for the esophagitis to completely heal and no surgery is required. Sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopolesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorders; arthritis; inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .
,
                                                                                                                                                                                                      Method for treatment of gastroesophageal reflux disease (GERD)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 49; DB 21; Length 11; Pred. No. 2.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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                                                                Michaeli D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAO00530 standard; Protein; 146 AA.
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                                                                                                                                                                                                                                                                              Example 4; Page 11; 24pp; English
                                                                Karr S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tang YT, Liu C, Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             65.3%;
80.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28-FEB-2000; 2000US-0515126.
18-MAY-2000; 2000US-0577409.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     06-NOV-2001 (first entry)
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                                                                Grimes S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-514838/56.
(APHT-) APHTON CORP
                                                                                                                                 WPI; 2000-062378/05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11 AA;
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The invention relates to human polynuclectides (AAI79941-AAI93841) and the encoded proteins (AAO00010-AAO13910) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynuclectides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, hematopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and extivity. Inhibin activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New nucleic acid molecules encoding 62 human secreted proteins for diagnosing, preventing, treating or ameliorating medical conditions and used as food additives or preservatives - \frac{1}{2} \int_{-\infty}^{\infty} \frac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Immunosuppressive; antiarthritic; antirheumatic; antiproliferative; cytostatic; cardiant; vasotropic; cerebroprotective; neuroprotective; nootropic; antibacterial; virucide; fungicide; opthalmalogical; human; vulnerary; gene therapy; infection; secreted protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fragment of human secreted protein encoded by gene 19 clone HTADW91.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Birse CE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Shi Y;
Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g., leukaemia, inflammation and immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
                                                                                                                                                                Claim 20; SEQ ID NO 14422; 1399pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 22; Length 146;
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Moore PA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2; Indels
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Florence KA,
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Pred. No. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB38442 standard; peptide; 383 AA.
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n HS, Ebner R,
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Olsen HS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2000-647418/62.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  146 AA;
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                                                                                           disorders
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Sequences AAB38321-B38396 represent the amino acid sequences of

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Whuman, cancer; ulcer; HIV infection; human immunodeficiency virus;
Mantinflammatory; antirheumatic; antiarthritic; immunosuppressive;
Mantibacterial; endocrine; cardiant; central nervous system: virucide;
anti-HIV; fungicide; antimutagen; cardiavascular; antianaemic; anaemia;
Matiaggregant; haemostatic; vulnerary; antiulcer; osteopathic; eczema;
Mermatological; antiallergic; antiasthmatic; antidiabetic; cytostatic;
Meuroprotective; antidepressant; nootropic; antiparkinsonian; infection;
Immunostimulant; gene therapy; antisense therapy; vaccine; inflammation;
Mantianaphylactic; rheumatoid arthritis; septic shock; pancreatitis;
Mantianaphylactic; neuropathology; cardiac anaphylaxis; autoimmunity;
Mantianaphylactic disease; haematopoietic disorder; platelet disorder; asthma;
Mirombocytopaenia; osteoporosis; severe combined immunodeficiency;
Mallergic rhinitis; diabetes; multiple sclerosis; depression;
Mallergic aliaease; Parkinson's disease; neurodegenerative disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                               ·;
human secreted proteins encoded by the genes AAC69512-C69587. The genes and proteins are useful for preventing, ameliorating or treating medical conditions, e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant)agonists are useful in the humantoid arthritis; (b) hyperproliferative discorders e.g. neoplasms of the breast or liver; (c) cardiovascular disorders e.g. neoplasms arrest; (d) cerebrovascular disorders e.g. cardiac arrest; (d) cerebrovascular disorders e.g. cerebral isolated anglogenesis; (f) nervous system disorders e.g. Alzhemia; (e) anglogenesis; (f) nervous system disorders e.g. Alzhemia; (e) infections caused by bacteria, viruses and fungi; and (h) ocular
                                                                                                                                                                                                                      disorders e.g. corneal infection. The polypeptides can also be used to ald wound healing and epithelial cell proliferation, to prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues and in
                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                     Score 49; DB 21; Length 383;
Pred. No. 62;
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                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human protein sequence SEQ ID NO:1128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAM25613 standard; Protein; 383 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                 65.3%;
80.0%;
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2000US-0488725.
2000US-0552317.
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                                                                                                                                                                                                                                                                                                                                                                                                                         8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         neurological disorder.
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N-PSDB; AAH99554.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        383 AA;
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21-JAN-2000;
25-APR-2000;
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                                                                                                                                                                                                                                                                                                       chemotaxis
                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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    δλ
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reatment and diagnosis of e.g. cancer, ulcers and HIV infection - xx

XX

S Claim 20; Page 234; 1217pp; English.

XX

C C AAM2966 to AAH99904 encode the human proteins given in AAM25225 to C AAM29966. The proteins can have activities based on the tissues and calls they are expressed in, such as: antiinfammatory; antirhenmatic; c antiarthritic; immunosuppressive; antibarcerial; endocrine; cardiant; c cardiovascular; antianemosuppressive; antibarcerial; antialematic; cardiovascular; antianemosuppressive; antidabetic; cytostatic; neuroprotective; antidepressant; nootropic; antidabetic; cytostatic; neuroprotective; antidepressant; nootropic; antidabetic; cytostatic; neuroprotective; antidepressant; nootropic; antidathem can be used in gene therapy, antisense therapy and vaccine production, The proteins and polynucleotides are useful for screening for agonists or antagonists of a protein and for the treatment and diagnosis c of disorders associated with the activity of a protein e.g. inflammation, neuropathology, cardiac anaphylaxis, viral, bacterial, HIV and fungal confections, autoimmunity, genetic disease, heamtopoletic disorders, cancer, multiple sclarosis, depression, costeoporosis, severe combined immunodeficiency, decreme, allergic continitis, asthma, diabetes, cancer, multiple sclarosis, depression, contended and disorders.

XX

Sequence 383 AA;

Sequence 383 AA;
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Search completed: February 5, 2003, 09:47:57 Job time : 36.4286 secs

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Gaps

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65.3%; Score 49; DB 22; Length 383; 80.0%; Pred. No. 62; 2; Indels Live 0; Mismatches 2; Indels

Query Match
Best Local Similarity 80.0°
Matches 8; Conservative

2 LGPQGRPPPP 11 ||| | ||||| 5 LGPPGSPPPP 14

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2003, 09:46:31 ; Search time 15.4286 Seconds (without alignments) 74.771 Million cell updates/sec
GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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Gapop 10.0 , Gapext 0.5
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75
1 ELGPQGRPPPPC 12
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Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR\_73:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

collagen alpha 1(X napin precursor (g conserved hypothethethypothethyp regulatory protein capsid protein - h collagen alpha 2(X HD protein - mouse hypothetical prote probable splicesos transcription fact homeotic protein H hypothetical protecollagen alpha 2(V hypothetical protecollagen alpha 2(V exopolysaccharide collagen alpha 1(V collagen alpha 1(X basic proline-rich proline-rich hypothetical prote proline-rich hypothetical prote proline-rich hypothetical protecollagen alpha 1(X basic proline-rich protecollagen alpha 1(X basic proline-rich protecollagen alpha 1(X basic proline-rich hypothetical protecollagen alpha 1(X basic proline-rich proline-rich proline-rich protecollagen alpha 1(X basic proline-rich protecollagen alpha 1(X basic proline-rich proline-rich protecollagen alpha 1(X basic proline-rich proline-rich proline-rich protecollagen alpha 1(X basic proline-rich proline Description SUMMARIES S23810 A29802 T02857 T32976 T29031 A47234 T13425 149729 D72654 A33509 T47181 B84565 I50589 T23561 A24450 T10216 A57131 S74742 A32856 S18251 CGHU1E C38355 D40750 D38355 S35941 П Query Match Length DB 1019 1024 1806 76 662.7 652.7 652.7 662.7 661.3 660.0 660.0 660.0 660.0 660.0 660.0 660.0 Score Result Ş.

E4 protein - human	salivary proline-r	proline-rich prote	Salivary proline-r	salivary proline-r	rhodopsin - Allote	rhodopsin [similar	rhodopsin - northe	transcription fact	Still frameshift 3	hypothetical profe	hypothetical profe	hypothetical prote	hypothetical profe	transcription acti	collagen alpha 1(v
W4WL5	PIHUPF	S10889	PIHUSD	PIHUB6	560755	529483	S14332	872233	E83250	T27136	T27135	T19140	T28897	A42091	сснити
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245	251	309	310	392	440	448	452	540	746	867	871	696	1001	1638	1838
58.7	58.7	58.7	58.7	58.7	58.7	58.7	58.7	58.7	58.7	58.7	58.7	58.7	58.7	58.7	58.7
44	44	44	44	44	44	44	44	44	44	44	44	44	44	44	44
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

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hypothetical protein F53G12.7 - Caenorhabditis elegans
C.Species: Caenorhabditis elegans
C.Species: Caenorhabditis elegans
C.Species: L5-Cat-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jan-2000
C.Accession: T29031
R.Wu, X.; Graves, T.
Submitted to the EMBL Data Library, May 1997
A.Description: The sequence of C. elegans cosmid F53G12.
A.Reference number: 22055
A.Accession: T29031
A.Accession: T29031
A.Accession: T29031
A.Reference number: L20532
A.Residues: DNA
A.Status: preliminary; translated from GB/EMBL/DDBJ
A.Residues: 1-327 <WUX>
A.Residues: 1-327 <WUX>
A.Residues: 1-327 <WUX>
A.Residues: 1-327 <WUX>
A.Residues: Sambi.AF003139; PIDN:AAB54156.1; GSPDB:GN00019; CESP:F53G12.7
A.Experimental source: EMBL:AF003139; Clone F53G12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Reference number: 221258
A; Reference number: 221258
A; Accession: 732976
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Residues: 1-211 <BEN>
A; Residues: 1-211 <BEN>
A; Residues: 1-211 <BEN>
A; Residues: 1-211 <BEN>
A; Experimental source: strain Bristol N2; clone F57H12
C; Genetics:
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C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 17-Oct-1997
                                                                                                                                                                                                                                                                                                                      hypothetical protein F57H12.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
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   Indels
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submitted to the EMBL Data Library, February 1998
A;Description: The sequence of C. elegans cosmid F57H12.
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   Mismatches
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A;Introns: 59/3; 138/1; 223/2
C;Superfamily: unassigned collagens
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Best Local Similarity 72.7.
Loc 8; Conservative
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Matches 7; Conservative
       Conservative
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260 EMGPQGPPGPP 270
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PRGGPPPPC 1863
                                                                         4 PQGRPPPPC 12
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A; Introns: 30/3; 159/3
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   7,
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       Matches
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NiAlternate names: 1.7 S seed storage protein
C;Species: Brassica napus (rape)
C;Date: 20-Jun-1989 #sequence_revision 20-Jun-1989 #text_change 16-Jul-1999
C;Accession: A29802
C;Accession: A29802
C;Accession: A29802
C;Accession: A29802
A;Title: Nucleotide sequence of a member of the napin storage protein family from Brassi
A;Reference number: A29802; MUID:87308225; PMID:3040733
A;Accession: A29802
A;Accession: A298
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A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Cross: 1-221 (eVL)
A;Cross-references: GB:AE001274; NID:93264850; PIDN:AAC24680.1; PID:93002479; GSPDB:GN0G
A;Experimental source: strain MHOM/IL/81/Friedlin
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C; Date: 24 Mar-1999 #sequence_revision 24-Mar-1999 #text_change 19-May-2000
C; Accession: E81463; T02867; T02867
R:Myler, P.J.; Audleman, L.; devos, T.; Hixson, G.; Kiser, P.; Lemley, C.; Magness, C.;
Proc. Natl. Acad. Sci. U.S.A. 96, 2902-2906, 1999
A; Title: Leishmania major Friedlin chromosome 1 has an unusual distribution of protein-ca. A; Reference number: A81455; MUID:99178987; PMID:10077609
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F;539-541/Region: cell attachment (R-G-D) motif
F;572-630/Domain: collagenous COL7 #status predicted <COL7>
F;572-530/Domain: collagenous COL6 #status predicted <COL6>
F;573-8-875/Domain: collagenous COL6 #status predicted <COL6>
F;738-875/Domain: collagenous COL3 #status predicted <COL5>
F;887-938/Domain: collagenous COL3 #status predicted <COL4>
F;1005-100/Region: cell attachment (R-G-D) motif
F;1011-1432/Domain: collagenous COL2 #status predicted <COL2>
F;1226-1228/Region: cell attachment (R-G-D) motif
F;127-157/Domain: collagenous COL1 #status predicted <COL1>
F;1472-157/Domain: collagenous COL1 #status predicted <COL1>
F;1578-1603/Domain: carboxyl-terminal nonhelical #status predicted
F;47,327/Binding site: carbohydrate (Asn) (covalent) #status predicted
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C;Superfamily: Leishmania major probable membrane protein L3162.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 50; DB 2; Length 1603;
Pred. No. 52;
1; Mismatches 1; Indels
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Pred. No. 9.6;
0; Mismatches
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88.9%;
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Best Local Similarity 80.0%;
Matches 8; Conservative
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Best Local Similarity 88.9
Matches 8; Conservative
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1280 MGPQGRPGPP 1289
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Best Local Similarity
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A;Reference number: A30083; MUID:88274327; PMID:2839594
A;Accession: H30084
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77.8%;
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Best Local Similarity
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A; Residues: 1-663 <ZHI>
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R;McGeoch, D.J.; Dalrymple, M.A.; Davison, A.J.; Dolan, A.; Frame, M.C.; McNab, D.; Perr J. Gen. Virol. 69, 1531-1574, 1988
A;Title: The complete DNA sequence of the long unique region in the genome of herpes sim
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              C; Accession: A47234
R; Stadler, H.S.; Padanilam, B.J.; Buetow, K.; Murray, J.C.; Solursh, M.
Proc. Natl. Acad. Sci. U.S.A. 89, 11579-11583, 1992
A; Title: Identification and genetic mapping of a homeobox gene to the 4p16.1 region of A; Reference number: A47234; MUID:93087572; PMID:1360670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R; Prost, E.; Deryckere, F.; Roos, C.; Haenlin, M.; Pantesco, V.; Mohier, E. Genes Dev. 2, 891-900, 1988
A; Title: Role of the oocyte nucleus in determination of the dorsoventral polarity of A; Reference number: A28826
A; Accession: A28826
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   regulatory protein K10, oocyte-specific - fruit fly (Drosophila melanogaster) N.Alternate names: protein EG:30B8.5 C.Species: Drosophila melanogaster C.Species: Drosophila melanogaster C.Species: Drosophila melanogaster C.Species: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 15-Oct-1999 C.Accession: T13425; A28826 R.Wurphy, L.; Harris, D.; Barrell, B. Submitted to the EMBL Data Library, April 1999 A:Description: Sequencing the distal X chromosome of Drosophila melanogaster. A.Reference number: 217668
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C;Date: 31-Dec-1989 #sequence_revision 31-Dec-1989 #text_change 16-Jun-2000
                                                                                                                                                                     Gaps
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A; Residues: 1-276, 'HH', 279-281, 'VDHHR', 287-463 <PRO>
A; Cross-references: GB:X12836; NID:98148; PID:9295771
                                                                                                                                                                                                                                                                                                                                                                  DB 2;
25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 47; DB;
Pred. No. 41;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        capsid protein - human herpesvirus 1 (strain 17)
                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                  Score 48;
Pred. No. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Cross-references: FlyBase: FBgn0000810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-463 <MUR>
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0
                                                                                                                                                                                                                                                                                                                                                               64.0%;
77.8%;
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70.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Gene: FlyBase:fs(1)K10
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278 MGPMGGPPPP 287
                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 7; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C; Keywords: DNA binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 LGPQGRPPPP 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 PQGRPPPPC 12
                                                                                                                                                      A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Accession: T13425
                                                                                                                                 A; Accession: A47234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Map position: X
A; Introns: 432/3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QQ
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A)My position: 6p21.3-6p21.3
A)Introns: 1302/3: 1332/3: 1332/3: 1350/3; 1440/1; 1477/3
A)Introns: 1302/3: 1332/3: 1332/3: 1350/3: 1440/1; 1477/3
A)Note: the list of introns is incomplete
C)Complex: type XI collagen may be a heterotrimer of two alpha 1(XI) chains (see PIR: 3(XI) chain (see PIR: GGHUGC), initially linked by disulfide bonds among their carbox remed with desmosine cross-links made from lysine and allysine residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Molecular cloning of cDNA and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A poscription: structural component of extracellular fibrous polymer associated with A;Note: may play a role in controlling the lateral growth of collagen II fibrils c. Superfamily: collagen alpha 1(V) chain; fibrillar collagen carboxyl-terminal homolociseywords: coiled coil; extracellular matrix; glycoprotein; hydroxylysine; hydroxypr F;1-254/Domain: non-collagenous (fragment) #status predicted <NC3> F;1-254/Domain: non-collagenous; triple ARP protein (fragment) #status predicted <PAR F;365-305/Domain: collagenous; triple halix #status predicted <CCL2> F;342/Domain: non-collagenous #status predicted <NC2> F;342/A31/Region: cell attachment (R-G-D) motif F;47-449/Region: cell attachment (R-G-D) motif F;1257-1259/Region: cell attachment (R-G-D) motif F;137-1259/Region: cell attachment (R-G-D) motif F;137-1380/Region: cell attachment (R-G-D) motif F;137-1380/Region: carboxyl-terminal nonhelical telopeptide F;1381-1546/Domain: carboxyl-terminal propebtide (fragment) #status predicted <CTP> F;1403-1546/Domain: fibrillar collagen carboxyl-terminal homology (fragment) #status
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R;Kimura, T.; Cheah, K.S.E.; Chan, S.D.H.; Lui, V.C.H.; Mattei, M.G.; van der Rest, J. Biol. Chem. 264, 13910-13916, 1989
A;Title: The human alpha2(XI) collagen (COLILA2) chain. Molecular cloning of CDNA an A;Reference number: A32645; MUID:89340485; PMID:2760050
                                                                                                                                                                                                                                                                                      A)Cross-references: GB:X14112; NID:g1944536; PIDN:CAA32318.1; PID:g59526; GB:D00317 C;Genetics: A,Gene: ULCs. And Came: ULCs. C;Superfamily: varicella-zoster virus gene 33 protein C;Superfamily: varicella-zoster virus gene 33 protein C;Superfamily: varicella-zoster virus gene 34 protein C;Superfamily: varicella-zoster virus gene 35 protein C;Superfamily: varicella-zoster virus gene 36 protein C;Superfamily: varicella-zoster virus gene 37 protein C;Superfamily: varicella-zoster virus gene 38 protein C;Superfamily: varicella-zoster virus gene 38 protein C;Superfamily: varicella-zoster virus gene 39 protein C;Superfamily: variet virus ge
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A;Residues: 586-1546 <KIM>
A;Cross-references: GB:J04974; NID:g180714; PIDN:AAA52034.1; PID:g180715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
0
A;Status: nucleic acid sequence not shown; translation not shown A;Molecule type: DNA
A;Residues: 1-635 <MCG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 635;
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Pred. No.
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A; cross-references: GB:J04804
C; Superfamily: meta-vinculin; vinculin amino-terminal homology; vinculin carboxyl-ter
C; Keywords: actin binding; cytoskeleton
F; 4-257, Domain: vinculin amino-terminal homology <VINN>
F; 4-277, Domain: vinculin carboxyl-terminal homology <VINC>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein DKF2p434F0616.1 - human (fragment)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 08-Dec-2000
C;Accession: T47181
R;Koehrer, K.; Beyer, A.; Mewes, H.W.; Weil, B.; Wiemann, S.
submitted to the Protein_Sequence Database, March 2000
                                                                                                                                                                                                                                                                                                                                                vinculin - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 22-Nov-1989 #sequence_revision 22-Nov-1989 #text_change 01-Mar-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                 C, Accession: A33509
R; Barstead, R.J.; Waterston, R.H.
J. Biol. Chem. 264, 10177-10185, 1989
A; Title: The basal component of the nematode dense-body is vinculin. A; Reference number: A33509; MUID:89255506; PMID:2498337
A; Accession: A33509
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                   Indels
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               5;
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53;
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               Mismatches
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Pred. No.
               0;
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C; Superfamily: POZ domain homology
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72.7%;
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70.08;
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Best Local Similarity 72.7
Matches 8; Conservative
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Best Local Similarity 70.0
Matches 7; Conservative
               Conservative
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A, Accession: T47181
A, Status: preliminary
A, Molecule type: mRnA
A, Residues: 1-315 <AAA>
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A; Residues: 1-1010 <BAR>
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                                                                                     4 PQGRPPPPC 12
                                                                                                                                                          71 POSRPPSPC 79
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               7;
               Matches
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D72654
hypotherical protein APE0664 - Aeropyrum pernix (strain KI)
C;Species: Aeropyrum pernix
C;Deteies: D72654
A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, A; Reference number: A72450; MUID:99310339; PMID:10382966
A;Accession: D72654
A;Accession: D72654
A;Molecule type: DNA
A;Residues: 1-112 < KAM>A;Accession: A7450; MUID:99310339; PMID:10382966
A;Cross-references: DDBJ:AP000060; NID:95104188; PIDN:BAA79636.1; PID:d1043422; PID:951C
C;Genetics:
A;Gene: APE0664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              H9 protein - mouse
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Accession: 149729; 149730
R;Lin, B.; Nasir, J.; MacDonald, H.; Hutchinson, G.; Graham, R.; Rommens, J.M.; Hayden, Hum. Mol. Genet. 3, 85-92, 1994
A;Tille: Sequence of the murine huntington disease gene: evidence for conservation and a A;Reference number: 149729; MUID:94214482; PMID:8162057
A;Accession: 149729
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Ccoss.references: GB:L23312; NID:9438804; PIDN:AAA37799.1; PID:9438805
A;Accession: 149730
A;Accession: 14
F;109-163,1511-1545/Disulfide bonds: #status predicted
F;319/Modified site: allysine (Lys) #status predicted
F;326,1266/Modified site: 5-hydroxylysine (Lys) #status predicted
F;426,1266/Modified site: carbohydrate (Lys) (covalent) #status predicted
F;927,933,1008,1017,1035,1038,1290,1296,1305,1317,1320/Modified site: 4-hydroxyproline (Pro) #status atypical
F;942,1023,1299/Modified site: 5-hydroxylysine (Lys) #status experimental
F;942,1023,1299/Modified site: carbohydrate (Lys) (covalent) #status experimental
F;1427,1433,1450,1459/Disulfide bonds: interchlain #status predicted
F;1460/Binding site: carbohydrate (Asn) (covalent) #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62.7%; Score 47; DB 2; Length 3119; 87.5%; Pred. No. 2.4e+02; ive 1; Mismatches 0; Indels
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Pred. No. 15;
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77.8%;
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Matches 8; Conservative
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Nature 402, 761-768, 1999

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transcription factor - chicken
C;Species: Gallus gallus (chicken)
C;Species: Gallus gallus (chicken)
C;Species: Gallus gallus (chicken)
C;Species: Gallus gallus (chicken)
C;Species: 13-599-1996 #sequence_revision 13-Sep-1996 #text_change 19-Jul-2002
C;Accession: 150589
R;Prince, V.; Lumsden, A.
Developement 120, 911-923, 1994
A;Title: Hoxa-2 expression in normal and transposed rhombomeres: independent regulation
A;Reference number: 150589; MUID:95324377; PMID:7600967
A;Reference number: 150589
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Rotous: preliminary; translated from GB/EMBL/DDBJ
A;Rotous: preliminary
A;Rotous: References: EMBL:X74323; NID:9415799; PIDN:CAA52370.1; PID:9415800
C;Genetics:
A;Genetics:
A;Genetics:
C;Superfamily: homeotic protein Hox B2; homeobox homology
C;Keywords: DNA binding; homeobox, nucleus; transcription regulation
F;141-197/Domain: homeobox homology <a href="https://www.nucleus">https://www.nucleus</a>; ranscription regulation
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: A84420; MUD:20083487; PMID:10617197
A:Reference number: B84565
A:Reference number: B84565
A:Rocession: B84565
A:Rolecule type: DNA
A:Rolecule type: DNA
A:Rolecule type: DNA
A:Residues: 1-363 <STO>
A:Cross-references: GB:AE002093; NID:g4218014; PIDN:AAD12222.1; GSPDB:GN00139
C:Genetics:
A:Gene: At2918510
A:Map position: 2
C:Superfamily: unassigned ribonucleoprotein repeat-containing proteins; ribonucleoprotei
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GenCore version Copyright (c) 1993 - 2003
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Q09457 caenorhabdi P25439 drosophila P20908 homo sapien O44431 drosophila O17482 drosophila P49021 drosophila P5932 mm musculu Q99372 rattus norv P15988 gallus gall P09853 herpes simp P05915 human immun	T.1  RAT.  RELEART STANDARD: PRT; 351 AA.  OBET58.  15-JUN-2002 (Rel. 41, Last sequence update)  16-JUN-2002 (Rel. 41, Last sequence update)  17-JUN-2002 (Rel. 41, Last sequence update)  18-JUN-2002 (R	2H2_1; 3. 2H2_2; 3. ator; 2inc-finger; Metal-binding; peat. LY-PRO. LY-PRO. LY-PRO. NC FINGERS. H2-TYPE. H2-TYPE. H2-TYPE. H2-TYPE. H2-TYPE.
CAEEL DROME L HUMAN DROHY DROWI DROME L CAEEL MOUSE RAT RAT L HV2V3	RT; 351 AP ence update) tation updat tation updat raniata; Ver ciurognathi; not defect. IN/GenBank/DD CC BOX IN THH GP Similar ar (By similar	
YQ36_CABEL BRM_DROME CA15_HUMAN TIM_DROHY TIM_DROVI TIM_DROME CC14_CAEEL CC14_CAEEL ELS_MOUSE ELS_MOUSE ELS_RAT CA26_CHICK RIR1_HSV23 VPX_HV2NZ	PRT;  ) guence notation ruppel ruppel sciur sciu	C2H2 C2H2 C2H2 C2H2 C2H2 POLY POLY POLY ZINC C2H2 C2H2 C2H2 C2H2
	Created) Last sequence to the contents of the	H2; 3. INGENINGER PACTURE LEID ACTURED PACTURED
963 1638 1838 1421 1421 345 860 860 11022	STANDARD:  1. 41, Created)  1. 41, Last see 2 (Lung kr  zoa; Ckat)  ria; Rodentia; 6; 6; 7. A. 8 K., Rothenbux he transcriptic t. T cells and i BB rats."; 6 K., Rothenbux 1. 4 Cells and i BB rats."; 7. A. 8 K., Rothenbux 1. A. 9 D. 1. Corranscriptic 1. Corranscriptic 1. Corranscriptic 1. Corranscriptic 1. Corranscriptic 1. Corranscriptic 1. Confit institution 1. Confit institutio	Znf_C2 F_C2H2 ZINC_F ZINC_F Jation ar pro ar pro 168 227 350 222 350 332 353
58.7 58.7 58.7 58.0 58.0 57.3 57.3 56.0	RAT STANDARD; PR 8; N-2002 (Rel. 41, Last seque N-2002 (Rel. 41, Last annot bel-like factor 2 (Lung Krug OR LKLF. S. norvegicus (Rat).	000003; 0355; Zn 200028; 200028; 10n regu 16 165 224 228 228 228 228 328
444 844 444	LT 1  RLE2_RAT STANDARD; PRT; 15-JUN-2002 (Rel. 41, Last sequence 16-JUN-2002 (Rel. 41, Last sequence 15-JUN-2002 (Rel. 41, Last sequence 15-JUN-2002 (Rel. 41, Last sequence 15-JUN-2002 (Rel. 41, Last sequence 11) SEQUENCE FROM N.A. STRAALSING (SCIUR NCELL) STRAALSING SCIUR 11) SEQUENCE FROM N.A. STRAALSING NO (BASTERS) SUDMITTED (AUG-1999) to the EMBL/GE 1- FUNCTION: BINDS TO THE CACCE BE AND ACTIVATES TRANSCRIPTION (BY-1- SUMILARITY: BELONGS TO THE KRUE FINGER PROPELIAS. This SWISS-PROT entry is copyright. 1- SUMILARITY: BELONGS TO THE KRUE 1- SIMILARITY: BELONGS TO THE KRUE 1- SUMICHES PROPELIAS.  This SWISS-PROT entry is copyright. 1- SUMICHES REQUIRES a license alreame 1- SHATBLES!; AAGO2141.1; 1- HSSP: POB047; 1SP2.	Probom; PD000003; Znf_C2H2; 2. SNART; SM00355; Znf_C2H2; 3. PROSITE; PS00028; ZNC_FINGER_C2H2_1; 3. PROSITE; PS50157; ZINC_FINGER_C2H2_2; 3. TRANSCTIPLION requlation; Activator; Zinc DNA-binding; Nuclear protein; Repeat. DOMAIN 165 168 POLY-PRO. DOMAIN 224 227 POLY-PRO. DOMAIN 268 350 ZINC FINGERE ZN_FING 268 292 C2H2-TYPE. ZN_FING 268 292 C2H2-TYPE. ZN_FING 328 350 C2H2-TYPE. ZN_FING 328 350 C2H2-TYPE. SEQUENCE 351 AA; 37313 MW; ZE4EB6805
000000044444 40000010040		
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Length 351;

DB 1;

Score 51;

68.08;

Query Match

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160 GPAGRPPPP 168
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                                                                                KLF2_HUMAN
                                                                    KLF2_HUMAN
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              ö
                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                  STRAIN-C57BL/6 X CBA; TISSUE-Lung;
MEDLINE-96052976; PubMed=756748;
Anderson K.P., Kern C.B., Crable S.C., Lingrel J.B.;
"Isolation of a gene encoding a functional zinc finger protein homologous to erythroid Kruppel-like factor: identification of a new multique family."
               Gaps
                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -1- SIMILARITY: BELONGS TO THE KRUEPPEL FAMILY OF C2H2-TYPE ZINC-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS00028; ZINC_FINGER_C2H2_1; 3.
PROSITE; PS0107; ZINC_FINGER_C2H2_2; 3.
Transcription regulation; Activator; Zinc-finger; Metal-binding; DNA-binding; Nuclear protein; Repeat.
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Pred. No. 5.9;
0; Mismatches 1; Indels
               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C4A99D018AC5BAF7 CRC64;
               ;;
                                                                                                                                                                 30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Kruppel-like factor 2 (Lung kruppel-like factor).
                                                                                                                                        354 AA
 No. 5.8;
              Mismatches
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ZINC FINGERS.
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C2H2-TYPE.
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POLY - PRO.
  Pred.
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MGD; MGI:1142772; K1f2.

Interpo, 1P000082; 2nf_C2H2.

Pfam; PF00096; zf-C2H2; 3.

PRINTS; PR000048; ZINCFINGER.

PRODOM; PD000003; Znf_CZH2; 3.

SMART; SM00355; ZnF_CZH2; 3.
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353 ZI
295 C2
325 C2
353 C2
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88.9%;
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 Similarity 88.9
8; Conservative
                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                     Mus musculus (Mouse)
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                                                          160 GPAGRPPPP 168
                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                         3 GPQCRPPPP 11
                                                                                                                                                                                                                                                                              NCBI_TaxID=10090;
                                                                                                                                                                                                                        KLFZ OR LKLF.
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                                                                                                                                      KLF2_MOUSE
Q60843;
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SEQUENCE
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GPQGRPPPP 11

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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kisselev L.L.;
"Structure of the human CpG-island-containing lung Kruppel-like factor (LKLF) gene and its location in chromosome 19p13.11-13 locus.";
FBBS Lett. 448:149-152(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wani M.A., Conkright M.D., Jeffries S., Hughes M.J., Lingrel J.B.; "CDNA isolation, genomic structure, regulation, and chromosomal localization of human lung kruppel-like factor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- SUBCELLULAR LOCATION: Nuclear (By similarity).
-!- SIMILARITY: BELONGS TO THE KRUEPPEL FAMILY OF C2H2-TYPE 2INC-
FINGER PROTEINS.
                                                                                                                                                                                                Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=99231781; PubMed=10217429;
Kozyrev S.V., Hansen L.L., Poltaraus A.B., Domninsky D.A.,
                                                                                                                                                                                                                                              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                         Q9Y573, Q9UKR6; Q9U355;
30-MAY-2000 (Rel. 39, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Kruppel-11ke factor 2 (Lung kruppel-like factor).
355 AA
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POLY-GLY.
POLY-PRO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=99389728; PubMed=10458913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL, AF123344; AAD25076.1; -. EMBL, AF13405; AAD5891.1; -. EMBL, AF205849; AAF13295.1; -. HSSP, p08047; 15P2.
     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genomics 60:78-86(1999).
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130
167
                                                                                                                                                                                                                                                                           NCBI_TaxID=9606;
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MIM; 602016;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     rissue=Lung;
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RA MEDLINE-93203161; PubMed=1284248;

RA Anamori T., Yamakoshi H., Nagai Y.;

RA Anamori T., Yamakoshi H., Nagai Y.;

RA Anamori T., Yamakoshi H., Nagai Y.;

T., Molecular cloning and partial characterization of a novel collagen to chain, alpha 1(XYI), consisting of repetitive collagenous domains and containing non-collagenous segments.";

J. Biochem. 112:856-863(1992).

C. I BIOCHOM. THE NUMEROUS INTERRUPTIONS IN THE TRIPLE HELIX MAY MAKE
C. I FUNCTION: THE NUMEROUS INTERUPTIONS IN THE AMNION. A MEMBRANOUS INTER CENTRY THE AMNIONI CAVITY. WITHIN THE COMPLEX NETWORK OF RETICULAR FIBERS. ALSO LOCATED TO A FIBROBLAST
C. LAYER BENEATH THIS DEBUSE LAYER. EXISTS IN TISSUES IN ASSOCIATION

CLAYER BENEATH THIS DEBUSE LAYER. EXISTS IN TISSUES IN ASSOCIATION
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                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-9233539; PubMed-1631157; Pan T.C., Zhang R.Z., Mattel M.-G., Timpl R., Chu M.-L.; "Cloning and chromosomal location of human alpha 1(XVI) collagen."; Proc. Natl. Acad. Sci. U.S.A. 89:6565-6569(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAINS (NCIO TO NCI).

PTM: PROLINES AT THE THIRD POSITION OF THE TRIPEPTIDE REPEATING UNIT (G-X-Y) ARE HYDROXYLATED IN SOME OR ALL OF THE CHAINS. SIMILARITY: BELONGS TO THE FIBRIL-ASSOCIATED COLLAGENS WITH, INTERRUPTED HELICES (FACIT) FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DEVELOPMENTAL STAGE: TRANSTENTLY ELEVATED EXPRESSION DURING GESTATION, AND DECREASE AT TERM.

DOMAIN: THIS SEQUENCE DEFINES EIGHTEEN DIFFERENT DOMAINS, NINE TRIPLE-HELICAL DOMAINS (COL9 TO COL1) AND TEN NONTRIPLE-HELICAL
                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                              ;
0
                                                                                                                           DB 1, Length 355; 7.9:
         ZINC FINGERS.

CZHZ-TYPE.

CZHZ-TYPE.

S -N (IN REF. | 2).

L -> P (IN REF. | 1).

E -> S (IN REF. | 2).

L -> M (IN REF. | 2).

L -> M (IN REF. | 2).

M; D5849C83ID676AEI CRC64;
                                                                                                                                                               1; Indels
                                                                                                                                                                                                                                                                                                         01-FEE-1995 (Rel. 31, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Collagen alpha 1(XVI) chain precursor.
                                                                                                                                                                                                                                                                          PRT; 1603 AA
                                                                                                                                                  Pred. No. 7.9; Mismatches
                                                                                                                                     Score 50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WITH OTHER TYPES OF COLLAGEN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 418-1603 FROM N.A. TISSUE=Placenta;
                                                                                                                                                                                                                                                                                                01-FEB-1995 (Rel. 31, Created)
                                                                                                             37419 MW;
                                                                                                                                    66.7%;
88.9%;
                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                        STANDARD;
3326
354
354
354
104
                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human)
                      272
302
332
43
104
175
355 AA;
                                                                                                                                    Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                 162 GPGGRPPPP 170
                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                    3 GPQGRPPPP 11
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                                                                                                                                                                                                                                                                      CA1F_HUMAN
Q07092;
                                             ZN_FING
CONFLICT
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CONFLICT
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DOMAIN
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SOLUTION
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Pressica napus (Rape).
Eukaryota: Viridiplantae: Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta: Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Brassica.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                         Extracellular matrix; Connective tissue; Collagen; Hydroxylation;
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0
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TRIPLE-HELICAL REGION 1 (COL1)
WITH 2 IMPERECTIONS.
NONHELICAL REGION 1 (NC1).
RDA -> GGR (IN REF. 2).
R -> P (IN DEF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAR-1989 (Rel. 10, Created)
01-MAR-1989 (Rel. 10, Last sequence update)
01-AUG-1992 (Rel. 23, Last annotation update)
Napin embryo specific precursor (1.7S seed storage protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TRIPLE-HELICAL REGION 3 (COL3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                         NONHELICAL REGION 5 (NC5).
TRIPLE-HELICAL REGION 4 (COL4)
WITH 2 IMPERFECTIONS.
                                                                                                                                                                                                     COLLAGEN ALPHA 1(XVI) CHAIN.
NONHELICAL REGION 10 (NC10).
TRIPLE-HELICAL REGION 9 (COL9)
                                                                                                                                                                                                                                                                                                                                                           NONHELICAL REGION 7 (NC7).
TRIPLE-HELICAL REGION 6 (COL6)
WITH 1 IMPERFECTION.
NONHELICAL REGION 6 (NC6).
                                                                                                                                                                                                                                                                                 TRIPLE-HELICAL REGION 8 (COL8) WITH 1 IMPERFECTION.
                                                                                                                                                                                                                                                                                                                NONHELICAL REGION 8 (NC8).
TRIPLE-HELICAL REGION 7 (COL7)
                                                                                                                                                                                                                                                                                                                                                                                                                          TRIPLE-HELICAL REGION 5 (COL5) WITH 3 IMPERFECTIONS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NONHELICAL REGION 3 (NC3).
TRIPLE-HELICAL REGION 2 (COL2)
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R -> P (IN REF. 2).

T -> P (IN REF. 2).

T -> P (IN REF. 2).

S -> P (IN REF. 2).

S -> P (IN REF. 2).

MW; E27D9AID4E598A37 CRC64;
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                                                                                                                                                                                                                                                                    (NC9)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 50;
Pred. No.
                                                                         InterPro; IPR000087; Collagen.
InterPro; IPR003129; TSPN.
EMBL; M92642; AAA58427.1; -. EMBL; S57132; AAB25797.1; -.
                                                                                                        Pfam; PF01391; Collagen; 18
Pfam; PF02210; TSPN; 1.
SMART; SM00210; TSPN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           157692
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                           PIR; S23810; S23810.
Genew; HGNC:2193; COL16A1.
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1603
374
505
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554
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722
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1010
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Best Local Similarity
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                                                          MIM; 120326; -
                                                                                                                                                                       Repeat; Signal
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MEDLINE=20196011; PubMed=10731137;
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                                                                                                                                                                                                                                         entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).

    Biol, Chem. 262:12202-12208(1987).
    FUNCTION: THE SMALL, BASIC, WATER-SOLUBLE NAPINS ARE ONE OF THE
TWO MAJOR KINDS OF STORAGE PROTEINS SYNTHESIZED IN THE SEED DURING

                                                                                                        -i- SUBUNIT: THE MATURE PROTEIN CONSISTS OF A SMALL AND A LARGE CHAIN LINKED BY DISULFIDE BONDS.
-i- TISSUE SPECIFICITY: COTYLEDONS AND THE AXIS.
-i- DEVELOPMENTAL STAGE: EMBRYO.
-i- SIMILARITY: BELONGS TO THE 2S SEED STORAGE ALBUMINS FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Drosophila melanogaster (Fruit fly).

Bukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

NCBI_TaxID=7227;
                        Scofield S.R., Crouch M.L.; Mullocotide sequence of a member of the napin storage protein family from Reserve and annual.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Role of the oocyte nucleus in determination of the dorsoventral polarity of Drosophila as revealed by molecular analysis of the K10 \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     65.3%; Score 49; DB 1; Length 186; 88.9%; Pred. No. 5.9; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Prost E., Deryckere F., Roos C., Haenlin M., Pantesco V.,
Mohier V.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   LARGE CHAIN.
9CAE63D84B160AB3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        K10_DROME STANDARD; PRT; 463 AA. P13468; 004675; 098605; 01-JAN-1990 (Rel. 13, Created) 15-JUL-1998 (Rel. 36, Last sequence update) 16-JUL-1998 (Rel. 36, Last sequence update) 16-OCT-2010 (Rel. 40, Last annotation update) 18-JUA-binding protein K10 (Female sterile protein K10). FS(1)K10 OR EG:30B8.5 OR CG3218.
                                                                                                                                                                                                                                                                                                  InterPro; IPR003612; AAI.
InterPro; IPR003612; Napin.
InterPro; IPR001768; Try/amyl_thhbtr.
Pfam; PF00234; tryp_alpha_amyl; 1.
PRINTS; PR00496; NAPIN.
PRODm; PD002498; Napin; 1.
SMARY; SM00499; AAI: 1.
Seed storage protein; Signal; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                            SMALL CHAIN.
           MEDLINE-87308225; PubMed-3040733;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                21013 MW;
                                                                                                                                                                                                                                                                               EMBL; J02782; AAA33007.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genes Dev. 2:891-900(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 65.3
Best Local Similarity 88.9
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                    186
                                                 from Brassica napus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 186 AA;
                                                                                                                                                                                                                                                                                            PIR; A29802; A29802
                                                                                             ITS MATURATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              97 GPQQRPPPP 105
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SEQUENCE FROM N.A.
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Remines P. W. Gairt M. K. Kabinier M. W. Marphy L. Harris D. Cadieue E. Barrell G., Perrac C. Viddal S. Brun C., Demailles T. Cadieue E. Barrell G., Perrac C., Viddal S., Brun C., Demailles T., Galbahov S., A Minana B. Kafetos E. C., Louis C., Siden Kimanos I., Bolshakov S., A Modole I. J. Peece A., Schoettler P., Mardines I. Bolshakov S., A Poppalannakis G., Spanos L., Cox S., Andenon E., & Ce Feblos B. A. Andenon E., Galliser C., Stanos L., Cox S., Andenon E., & Ce Feblos B. A. Galliser D. M. Campbell L.A., Schoettler P., Martines I. B., Souders R.D. C., Martines I. M. Peece A., Schoettler P., Martines I. M. Bourkloif F., Sauders R.D. C., Martines I. M. Bourkloif F., Sauders R.D. C., Martines I. M. Bourkloif F., Bourders R.D. C., Martines I. M. Bourkloif F., Bourders R.D. C., Martines I. M. Bourkloif F., Bourders R.D. C., Martines I. M. Bourkloif F., Bourder B. M. B., Martines R.D. C., Martines E., Martines I. M. Bourkloif S. M. Sabhurar M. Heddiston S. P. K. Martines R.D. C., Martines F. L., Sabhurar M. Heddiston S. M. Martines R.D., Cabines F., Martines R.D., Cabines P. M., Martines R.D., Martines
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CHAIN
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                                                                                                                                                                      Coat
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            DORRADOR STATE TO THE SOLUTION OF THE STATE THE SOLUTION OF TH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAR-1989 (Rel. 10, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Capsid protein P40 (Virion structural protein UL26) [Contains: Capsid
Protein VP24 (Assemblin) (Protease) (EC 3.4.21.97); Capsid protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-88274327; Pubmed-2839594; McGeoch D.J., Dalrymple M.A., Davison A.J., Dolan A., Frame M.C., McNab D., Perry L.J., Scott J.E., Taylor P.; Mrab Complete DNA sequence of the long unique region in the genome of herpes simplex virus type 1."; J. Gen. Virol. 69:1531-1574(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Davison M.D., Rixon F.J., Davison A.J.;
"Identification of genes encoding two capsid proteins (VP24 and VP26) of herpes simplex virus type 1.";
of herpes simplex virus type 1.";
J. Gen. Virol. 73:2709-2713(1992).
J. Gen. Virol. 73:2709-2713(1992).
PROCESSING AND PACKAGING OF PROGENY DNA. VP24 IS A PROTEASE WHICH CAN PROTEOLYTICALLY CLEAVE ITSELF AND VP22A AT THE C-
                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CATALYTIC ACTIVITY: Preferentially cleaves at Ala-|-Ser or Ala-|-
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0
                        X APPROXIMATE TANDEM REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY: BELONGS TO PEPTIDASE FAMILY S21.
SIMILARITY: TO OTHER HERPESVIRUSES CAPSID PROTEIN VP40
                                                                                                                                                                                                                                                                                                                                                    Score 47; DB 1; Length 463;
                                                                                                                                                                                                                                                   PM -> HH (IN REF. 1).
GGPPP -> VDHHR (IN REF. 1).
D03C097192D1FDD0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                  2; Indels
                                                                                                                                                                                                          POLY-PRO.
H-T-H MOTIF (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Herpes simplex virus (type 1 / strain 17).
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Alphaherpesvirinae; Simplexvirus.
NCBI_TaxID=10299;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          635 AA
                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                       Pred. No.
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    Repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PTM: VP22A IS PHOSPHORYLATED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAR-1989 (Rel. 10, Created)
                                                                                                                                                                                                                                                                                                      MM;
                                                                                                                                                                                                                                                                                                                                             62.7%;
                                                                                                                                                                                                                                                                                                                                                                       70.08;
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                                                                                                                                                                                                                                                                                                      51267
                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
  Nuclear
                                                                                                                                                                                                                                                                         282
463 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    278 MGPMGGPPPP 287
                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                         2 LGPQGRPPPP 11
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                        87
87
95
110
111
127
127
284
3397
DNA-binding;
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P10210;
                                                                                                                                                                                                      DOMAIN
DNA_BIND
CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                            THE PROTEASE) (PROBABLE).
SYSTEM (BY SIMILARITY).
SYSTEM (BY SIMILARITY).
SYSTEM (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                    C-TERMINAL PEPTIDE.
CLEAVAGE (BY THE PROTEASE) (PROBABLE)
CLEAVAGE (BY THE PROTEASE) (PROBABLE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rowen L., Qin S., Madan A., Loretz C., James R., Dors M., Mix L.,
Hall J., Lasky S., Hood L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'Sequence of the mouse major histocompatibility locus class II
                                                                                                                                                                                                                                                                    (PROTEASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- SIMILARITY: BELONGS TO THE FIBRILLAR CLASS OF COLLAGENS.
                                                                                                                                                                                      protein; Hydrolase; Serine protease; Phosphorylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1; Length 635;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         F3B3C7D42F3D062D CRC64;
                                                                                                                                                                                                                                                                 CAPSID PROTEIN VP24 (CAPSID PROTEIN VP22A.
                                                                                                                                                                                                                  GENE UL26 PROTEIN.
GENE UL26.5 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       064739; 0921W0;
15-JUL-1998 (Rel. 36, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Collagen alpha 2(XI) chain precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1650 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                     CHARGE RELAY
CHARGE RELAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          CHARGE RELAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                        MEROPS; S21.001; ...
InterPror; IRROU847; Assemblin.
Pfam; PF00716; Peptidase_S21; 1.
PRINTS; PR00236; HSVCAPSIDP40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   66470 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               77.88;
EMBL; X14112; CAA32318.1;
PIR; H30084; WMBEW6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
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129
148
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247
?610
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248
611
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
nes 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                635 AA;
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565 PPGPPPPC 573
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129
148
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                                                     HSSP; P16753;
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ACT_SITE
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SEQUENCE
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PROPEP
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SECUENCE OF
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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "The human COL11A2 gene structure indicates that the gene has not
                                                                                                                                                                                                 Extracellular matrix; Connective tissue; Repeat; Hydroxylation; Glycoprotein; Collagen; Alternative splicing; Signal. SIGNAL 1 22 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   evolved with the genes for the major fibrillar collagens.";
                                                                                                                                                                                                                                                                                                                                                                                               DB 1; Length 1650;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE-96032717; PubMed-7559422;
Vuoristo M.M., Pihlajamaa T., Vandenberg P., Prockop D.J.,
                                                                                                                                                                                                                                     CARBOXYL-TERMINAL PROPEPTIDE
                                                                                                                                                                                                                                                                                                                                                                      • M (IN REF. 2).
8ECDB8702E71E2DA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                 POTENTIAL. COLLAGEN ALPHA 2(XI) CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CA2B_HUMAN STANDARD; PRT; 1736 AA. P13942; 013273; 013271; 013272; 007751; 099866; 09UIP9; 01-JAN-1990 (Rel. 13, Created) 16-OCA--1990 (Rel. 40, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                           NONHELICAL REGION.
R -> L (IN REF. 2).
NQ -> KP (IN REF. 2).
V -> A (IN REF. 2).
TGP -> HGS (IN REF. 2).
                                                                                                                                                                                                                                            NONHELICAL REGION.
TRIPLE-HELICAL REGION.
                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                Score 47;
Pred. No.
                                                                     MGD; MGI:88447; COIlla2.
InterPro; IPR000087; Collagen.
InterPro; IPR0000885; Fib_collagen_C.
InterPro; IPR001791; Laminin_G.
InterPro; IPR001230; Prenyl_site.
InterPro; IPR0013129; TSPN.
Pfan; PF01391; Collagen; 18.
Pfan; PF01310; COLFI: 1.
ProDom; PF002077; Fib_collagen; 4.
ProDom; PD0020778; Fib_collagen_C; 1.
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                                                                                                                                                                                                                                                                                                                                                                                               62.7%;
80.0%;
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                                                                                                                                                                               SM00282; LamG; 1
SM00210; TSPN; 1
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553 LGPQGEPGPP 562
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Best Local
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Matches
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Zhidkova N.I., Brewton R.G., Mayne R.; "Molecular cloning of PARP (proline/arginine-rich protein) from human cartilage and subsequent demonstration that PARP is a fragment of the NH2-terminal domain of the collagen alpha 2(XI) chain."; FEBS Lett. 326:25-28(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 730-1690 FROM N.A.
MEDLINE=83340485; Pubmed=2760050;
Kimura T., Cheah K.S.E., Chan S.D.H., Lui V.C.H., Mattei M.-G.,
van der Rest M., Ono K., Solomon E., Ninomiya Y., Olsen B.R.;
"The human alpha 2(XI) collagen (COLILA2) chain. Molecular cloning of cDNA and genomic DNA reveals characteristics of a fibrillar collagen with differences in genomic organization.";
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Kuivaniemi H., Tromp G., Prockop D.J.;
"Mutations in fibrillar collagens (types I, II, III, and XI), fibrill-
associated collagen (type IX), and network-forming collagen (type X)
cause a spectrum of diseases of bone, cartilage, and blood vessels.";
Hum. Mutat. 9:300-315(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lui V.C., Ng L.J., Sat E.W., Cheah K.S.;
"The human alpha 2(XI) collagen gene (COL11A2): completion of coding information, identification of the promoter sequence, and precise localization within the major histocompatibility complex reveal Genomics 32:401-412(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Melkoniemi M., Brunner H.G., Manouvrier S., Hennekam R., Superti-Furga A., Kaeaeriaeinen H., Pauli R.M., van Essen T., Warman M.L., Bonaventure J., Miny P., Ala-Kokko L.; "Autosomal recessive disorder otospondylomegaepiphyseal dysplasia is associated with loss-of-function mutations in the COL11A2 gene.";
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MEDLINE=95163096; PubMed=7859284;
Vikkula M., Mariman E.C.M., Lui V.C.H., Zhidkova N.I., Tiller G.E., Goldring M.B., van Beersum S.E.C., de Waal Malefijt M.C., van den Hoogen F.H.J., Ropers H. H., Mayne R., Cheah K.S.E., Olsen B.R., Warman M.L., Brunner H.G.;
"Autosomal dominant and recessive osteochondrodysplasias associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Koga H., Sakou T., Taketomi E., Hayashi K., Numasawa T., Harata S., Yone K., Matsunaga S., Otterud B., Inoue I., Leppert M.; "Genetic mapping of ossification of the posterior longitudinal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ALTERNATIVE SPLICING.
MEDLINE-95238468; PubMed-7721876;
Zhidkova N.I., Justice S.K., Mayne R.;
Talternative mRNA processing occurs in the variable region of the pro-alpha 1(XI) and pro-alpha 2(XI) collagen chains.";
J. Biol. Chem. 270:9486-9493(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VARIANTS GLY-593; LYS-824; LEU-879; THR-1316 AND GLN-1600
                                                                                                                                                         Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.
Biol. Chem. 270:22873-22881(1995)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 1-537 FROM N.A.
MEDLINE=96435918; PubMed=8838804;
                                                                                                                                                                                                                                                                                                                                         MEDLINE=93314796; PubMed=8325374;
                                                                                                                                                                                                                                                 59-807 FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ligament of the spine.";
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                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                      rissum=cartilage;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PubMed=10677296;
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62.7%; Score 47;
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ProDom; PD000007; Collagen; 1.
ProDom; PD002078; Fib_collagen_C; 1.
SMART; SM00038; COLFT; 1.
SMART; SM00282; LamG; 1.
SMART; SM00210; TSPN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR000087; Collagen.
InterPro; IPR0000885; Fib_collagen_C.
InterPro; IPR001791; Laminin_G.
InterPro; IPR001230; Prenyl_site.
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                                                                                                                                              EMBL, U32169; AAC50214.1; -.
EMBL, U32169; AAC50213.1; -.
EMBL, U32169; AAC50215.1; -.
EMBL, AL03128; CAA2024.1; -.
EMBL, L18987; CAA2024.1; -.
EMBL, J04974; AAA52034.1; -.
EMBL, U41065; AAC17464.1; JOINED.
EMBL, U41065; AAC17464.1; JOINED.
EMBL, U41066; AAC17464.1; JOINED.
EMBL, U41067; AAC17464.1; JOINED.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF01391; Collagen; 18.
Pfam; PF01410; COLFI; 1.
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Matches 8; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MIM; 215150; -.
MIM; 277610; -.
MIM; 601868; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MIM; 184840; -.
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P51111;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Genew;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -1. DISEASE: Defects in COL11A2 are the cause of autosomal recessive otospondylomegaepiphyseal dysplasia (OSMED), a skeletal dysplasia accompanied by severe hearing loss. The phenotype overlaps that of autosomal dominant skeletal disorders (Stickler and Marshall syndromes) but can be distinguished by disproportionately short limbs and lack of coular involvement.

-1. DISEASE: Defects in COL11A2 are the cause of Weissenbacher.

Zweymueller syndrome (WZS), an autosomal dominant disorder allelic with STL3 and OSMED. It is also referred to as heterozygous OSMED.
-1. DISEASE: Defects in COL11A2 are the cause of autosomal dominant nonsyndromic sensorineural deafness type 13 (DFNA13). Affected individuals experience progressive hearing loss beginning in the second to fourth decades, eventually making use of amplification
                                                                                                                      Gledion A., Wiesbauer P., Spranger J., Ala-Kokko L.; "Heterozygous glycine substitution in the COL11A2 gene in the original patient with the Weissenbacher-Zweymueller syndrome demonstrates its identity with heterozygous OSMED (nonocular Stickler syndrome)."; Am. J. Med. Genet. 80:115-120(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CONTROLLING LATERAL GROWTH OF COLLAGEN II FIBRILS. SUBUNIT: TRIMERS COMPOSED OF THREE DIFFERENT CHAINS: ALPHA 1(XI), ALPHA 2(XI), AND ALPHA 3(XI). ALPHA 3(XI) IS A POST-TRANSLATIONAL MODIFICATION OF ALPHA 1(II). ALPHA 1(V) CAN ALSO BE FOUND INSTEAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AMOUNTS:
DEFASE: Defects in COL11A2 are the cause of Stickler syndrome type 3 (STL3). It is an autosomal dominant disorder characterized by oro-facial, auditory and skeletal manifestations, such as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            midfacial hypoplasia, cleft palate, osteoarthritis, and sensorineural hearing loss. Differently from Stickler syndrome type 1 and 2, no ocular involvement is observed. This disorder is also referred to as Stickler-like syndrome or non-ocular Stickler
                                                                                                                                                                                                                                                                                                                            Sirko-Osadsa D.A., Murray M.A., Scott J.A., Lavery M.A., Warman M.L., Robin N.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OF ALPHA 3(XI)=1(II).

ALTERNATIVE PRODUCTS: 8 isoforms; 1 (shown here), 2, 3, 4, 5, 6, and 8: way be produced by alternative splicing. They lack exons 6 7 or 8 or a combination of these exons. PTM: PROLINES AT THE THIRD POSITION OF THE THEEPTIDE REPEATING UNIT (G-X-Y) ARE HYDROXYLATED IN SOME OR ALL OF THE CHAINS. PTM: A DISULEIDE-BONDED PEPTIDE CALLED PROLINE/ARGININE-RICH PROTEIN OR PARP IS RELEASED FROM THE AMINOT TERMINISD DURING
                                                                                                                                                                                                                                                                                                                                                                            "Stickler syndrome without eye involvement is caused by mutations in COL11A2, the gene encoding the alpha-2(XI) chain of type XI collagen.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VARIANTS DFNA13 GLU-808 AND CYS-1034, AND REVISIONS TO 1031-1032.
MEDLINE-20047768; PubMed-10581026;
MCGUITW M.T., PRASAG S.D., Griffith A.J., Kunst H.P.M., Green G.E., Shpargel K.B., Runge C., Huybrechts C., Mueller R.F., Lynch E., King M.-C., Brunner H.G., Cremers C.W.R.J., Takanosu M., Li S.-W., Arita M., Mayne R., Prockop D.J., Van Camp G., Smith R.J.H.;
"Mutations in COL11A2 cause non-syndromic hearing loss (DFNA13).";
Nat. Genet. 23:413-449 (1999).
-! FUNCTION: MAY PLAY AN IMPORTANY ROLE IN FIBRILLOGENESIS BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EXTRACELLULAR PROCESSING AND IS SUBSEQUENTLY RETAINED IN THE CARTILAGE MATRIX FROM WHICH IT CAN BE ISOLATED IN SIGNIFICANT
                                                                                                 Pihlajamaa T., Prockop D.J., Faber J., Winterpacht A., Zabel B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASS OF COLLAGENS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WWW="http://www.uia.ac.be/dnalab/hhh/hhhgenes.html".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DATABASE: NAME-Hereditary hearing loss homepage;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY: BELONGS TO THE FIBRILLAR
J. Hum. Genet. 62:1460-1467(1998)
                                                                                                                                                                                                                                                                             VARIANT STL3 940-GLY--PRO-948 DEL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pediatr. 132:368-371(1998).
                                                  VARIANT WZS GLU-955.
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                                                                    PubMed=9805126;
                                                                                                                                                                                                                                                                                                       PubMed=9506662;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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01-0CT-1996 (Rel. 34, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Huntingtin (Huntington's disease protein homolog) (HD protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .;
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Hameister H., Epplen J.T., Riess O.;
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Mismatches
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                                                                                -: SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-: TISSUE SPECIFICITY: EXPRESSED TO A HIGH DEGREE IN ALL THE REGIONS OF THE BRAIN OF ADULTS AND IN MEIOTIC CELLS OF THE TESTIS. IN ADDITION, VERY LOW LEVELS ARE DETECTED IN VARIOUS NON-NEURONAL TISSUES (HEART, MOSCLE, LIVER, LUNG AND KIDNEY).
-: DEVELOPMENTAL STAGE: IDENTIFIED AT HIGH LEVELS IN NEURONAL TISSUES OF EMBRYOS AS EARLY AS DAY 14.5. THIS EXPRESSION REMAINS CONSTANT IN ALL FURTHER DEVELOPMENT STAGES (UP TO THE ADULT). ON THE OTHER HAND THE EXPRESSION IN NON-NEURONAL TISSUES IS DOWN-REGULATED FROM STAGE 17.5 DAY OLD EMBRYOS.
Strong T.V., Tagle D.A., Valdes J.M., Elmer L.W., Boehm K., Swaroop M., Kaatz K.W., Collins F.S., Albin R.L.; "Widespread expression of the human and rat Huntington's disease gene in brain and nonneural tissues.";
                                                                                                                                                                                                          -!- POLYMORPHISM: THE POLY-GLN REGION DOES NOT APPEAR TO BE POLYMORPHIC, EXPERINING THE ABSENCE OF A RODENT HD-LIKE DISORDER.
-!- SIMILARITY: CONTAINS 10 HEAT REPEATS.
-!- SIMILARITY: BELONGS TO THE HUNGTINTIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                               Nat. Genet. 5:259-265(1993).
-!- FUNCTION: MAY PLAY A ROLE IN MICROTUBULE-MEDIATED TRANSPORT OR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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01-OCT-1996 (Rel. 34, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Huntingtin (Huntington's disease protein homolog) (HD protein)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 47; DB 1; Length 3110;
Pred. No. 1.4e+02;
1; Mismatches 0; Indels
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STAIN-CSTBL/G: TISSUE-Brain, and Spleen:
MEDIINE-94214482; Pubmed-8162057;
Lin B., Nasir J., Macdonald H., Hutchinson G., Graham R.K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        33C357E8FC141550 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                          REPEATS DOMAIN 1. REPEATS DOMAIN 2. REPEATS DOMAIN 3.
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POLY-GLN.
POLY-PRO.
POLY-PRO.
POLY-THR.
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EMBL; U01022; AAC52133.1; -.
InterPro: IPR000091; Huntingtin.
Pfan; PF03541; Huntingtin; 1.
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PRINTS; PR00375; HUNTINGTIN.
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87.5%;
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Best Local Similarity 87.5.
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                                                                         VESICLE FUNCTION.
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38 PQGQPPPP 45
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2606
3110
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P42859;
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                                                                                                                conservation, alternate splicing and polymorphism in a triplet (CCG)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Goldberg Y.P., Hayden M.R.; "Structural analysis of the 5' region of mouse and human Huntington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               disease genes reveals conservation of putative promoter region and di- and trinucleotide polymorphisms."; Genomics 25:707-715(1995).

-i- FUNCTION: MAY PLAY A ROLE IN MICROTUBULE-MEDIATED TRANSPORT OR VESICLE FUNCTION.
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Barnes G.T., Duyao M.P., Ambrose C.M., McNeil S., Persichetti F., Strindhi J., Gusella J.F., Macdonald M.E.; "Mouse Huntington's disease gene homolog (Hdh)."; Somat. Cell Mol. Genet. 20:87-97(1994).
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SEQUENCE FROM N.A.
MEDLINE-95375771; PubMed=7647777;
Trottier Y., Devys D., Imbert G., Saudou F., An I., Lutz Y.,
Weber C., Agid Y., Hirseh B.C., Mandel J.L.;
"Cellular localization of the Huntington's disease protein and
discrimination of the normal and mutated form.";
Nat. Genet. 10:104-110(1995).
Rommens J.M., Hayden M.R.; "Sequence of the murine Huntington disease gene: evidence for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 1-181 FROM N.A.
MEDLINE-95278941; PubMed=7759106;
Lin B., Nasir J., Kalchman M.A., McDonald H., Zeisler J.,
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Alternative splicing; Polymorphism; Repeat.
DOMAIN 182 306 HEAT REPEATS D
DOMAIN 723 920 HEAT REPEATS D
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L28827; AAA89100.1; ALT_SEQ.
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MEDLINE=94278649; Pubmed=8009370;
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                                                                                                                                                                                                                     Hum. Mol. Genet. 3:85-92(1994).
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                                                                                                                                                                                                                                                                                                          Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T., Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Ota T., Suzuki Y., Obayashi M., Nishi T., Shibahara T., Tanaka T., Nakamura Y., Isogai T., Sugano S.; Nishi T., Shibahara T., Tanaka T., Nakamura Y., Isogai T., Sugano S.; Nishi T., Sugano S.; Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
--- SUBUNIT: Interacts with topoisomerase 1.
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Rhabditidae; Peloderinae; Caenorhabditis.
                                                            s:
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                                                   Wiemann S., Weil B., Wellenreuther R., Gassenhuber J., Glassl S Ansorge W., Boecher M., Bloecker H., Bauersachs S., Blum H., Lauber J., Duesterhoeft A., Beyer A., Koehrer K., Strack N., Mewes H.-W., Ottenwealder B., Obermaier B., Tampe J., Heubner Wambutt R., Korn B., Klein M., Poustka A.; "Towards a catalog of human genes and proteins: sequencing and analysis of 500 novel complete protein coding human cDNAs."; Genome Res. 11:422-435(2001).
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C -> G (IN REF. 2).
L -> P (IN REF. 4).
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01-FEB-1991 (Rel. 17, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       skeletal muscle.
-!- SIMILARITY: CONTAINS 1 BTB/POZ DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No.
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TISSUE=Testis;
MEDLINE=21154917; PubMed=11230166;
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STRAIN=Bristol N2;
MEDLINE=8925506; Pubmed=2498337;
Barstead R.J., Waterston R.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genew; HGNN:11120, DIDGE.
InterPro; IPR000210; BTB_POZ.
Pfam; PF00651; BTB; 1.
PROSITE; PS50097; BTB; 1.
DOMAIN 69 145 BT
CONFLICT 406 T
CONFLICT 422 422 C
CONFLICT 429 429 L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL, AL136853; CAB66787.1; ... EMBL, AF355402; AAK25855.1; ... EMBL, AF257241; AAK17068.1; ... EMBL, AK000731; BAA91345.1; ... Genew; HGNC:1120; BTBD1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     52771 MW;
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Matches 8; Conserv
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P19826;
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Yang L., Xu L., D'Arpa P.;
"Characterization of two similar BTB-containing Kelch-like proteins,
BTBD1 and BTBD2, identified as topoisomerase I-interacting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Carim-Todd L., Sumoy L., Andreu N., Estivill X., Escarceller M.; identification and characterization of BTBD1, a novel BTB domain containing gene on human chromosome 15q24."; Gene 262:275-281(2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MW; ECA42B5916F50F4F CRC64;
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REPEATS DOMAIN 3.
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A -> P (IN REF. 1).
A -> P (IN REF. 1).
A -> P (IN REF. 1).
D -> E (IN REF. 1).
D -> E (IN REF. 1).
T -> N (IN REF. 1).
D -> G (IN REF. 1).
D -> G (IN REF. 1).
C -> G (IN REF. 1).
D -> G (IN REF. 1).
C -
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SEQUENCE FROM N.A.
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45 PQGQPPPP 52
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SEQUENCE
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                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                 -!- SUBUNIT: EXHIBITS SELF-ASSOCIATION PROPERTIES.
-!- SUBCELLULAR LOCATION: CYTOPLASMIC FACE OF ADHESION PLAQUES.
-!- SIMILARITY: STRONG, TO OTHER VINCULINS AND TO ALPHA-CATENINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; Irrodocats; vinculing and interpro; Irrodocats; vinculing and interpro; Irrodocats; vinculing 1.

PRINTS; PROBOGS; VINCULIN 2.

PROSTE; PSO0663; VINCULIN 2; 2.

PROSTE; PSO0664; VINCULIN 1; 1.

PROSTE; PSO0664; VINCULIN 2; 2.

Cell adhesion; Actin binding; Cytoskeleton; Structural protein; Phosphorylation; Repeat.
"The basal component of the nematode dense-body is vinculin."; J. Biol. Chem. 264:10177-10185. [AB9].
-!- FUNCTION: INVOLVED IN CELL ADBESTON. MAY BE INVOLVED IN THE ATTACHMENT OF THE ACTIN-BASED MICROFILAMENTS TO THE PLASMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0
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111922 MW; DAF789EA4C786721 CRC64;
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Pred. No. 66; 3; Indels
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SIMILARITY: BELONGS TO THE ANTP HOMEOBOX FAMILY.
PROBOSCIPEDIA SUBFAMILY.
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01-0CT-1994 (Rel. 30, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
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MEDLINE-95324377; PubMed=7600967;
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Matches 8; Conserv
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Q08727;
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the Buropean Bioinformatics Institute. There are no restrictions on its
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or send an email to license@isb-sib.ch).
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15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Hypermethylated in cancer 2 protein (Hic-2) (Hic-3) (HIC1-related gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Alliel P.M., Goudou D., Bitoun M., Seddigi N., Rieger F., Perin J.-P., "Complete deduced structure of HIC-3, a novel human btb/poz and zF factor of the HIC family.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Dunham I., Hunt A.R., Collins J.E., Bruskiewich R., Babbage A.K., Calamp M., Smink L.J., Alnscough R., Almelda J.P., Babbage A.K., Bagguley C., Bailey J., Barlow K.F., Bates K.N., Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Buck D., Burgess J., Bridgeman A.M., Buck D., Burgess J., Carder C., Carter N.P., Chen Y., Clark G., Clegs S.M., Cobley V.E., Cole C.G., Collier R.E., Connor R., Conroy D., Corby N.R., Coville G.J., Cox A.V., Davis J., Dawson E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Deltour S., Pinte S., Guerardel C., Leprince D.; "Characterization of HRG22, a human homologue of the putative tumor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 1-85 FROM N.A. (ISOFORM 1), AND ALTERNATIVE SPLICING MEDLINE=21438979; PubMed=11554746;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homeobox; DNA-binding; Developmental protein; Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 45; DB 1; Length 375; Pred. No. 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C7C4CA10455C3B11 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ANTP-TYPE HEXAPEPTIDE. HOMEOBOX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             suppressor gene HIC1.";
Biochem. Biophys. Res. Commun. 287:427-434(2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             615 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                  HASP, F44633, 1267.

TRANSFAC, T01700, -
InterPro; IPR001862, Honeobox.
InterPro; IPR001865, Homeobox.
Fam; PR00046, homeobox. 1.
PRINTS; PR00024; HOMEOBOX.
PRODOM; PD000014, HOMEOBOX.
PRODOM; P0000104, HOMEOBOX.
PROSTE; SM0389; HOX; 1.
PROSTE; PS50071; HOMEOBOX.2; 1.
PROSTE; PS50071; HOMEOBOX.2; 1.
PROSTE; PS50031; HOMEOBOX.2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=20057165; PubMed=10591208;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. (ISOFORM 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  40998 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          60.08;
77.88;
                                                                                                                                                            EMBL; X74323; CAA52370.1; -. HSSP; P14653; 1B72.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              on chromosome 22).
HIC2 OR HRG22 OR KIAA1020.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Transcription regulation.
NOMAIN 94 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 77.8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                375 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 GPQGRPPPP 11
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EMBL; AL162003; CAB82344.1;

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RA Dhami P.D., Dockree C., Dodsworth S.J., Durbin R.M., Ellington A.G.,
RA Gilbert JG.R., Fewy J.M., Fleming K., French L., Garner A.A.,
Gilbert JG.R., Goward M. E., Grafham D.V., Griffiths M.N.D., Hall C.,
RA Hall R.E., Hall-Tamlyn G., Heathcott R.W., Ho S., Holmes S.,
Laird G.K., Langford C.F., Leversha M.A., Lloyd C., Lloyd D.M.,
RA Martyn I.D., Mashreqhi-Wohammadi M., Matthews L.H., Morcann O.T.,
RA Martyn I.D., Mashreqhi-Wohammadi M., Matthews L.H., Morcann O.T.,
RA Martyn I.D., Pewritt R., Pearce A.V., Pearson D., Phillimore B.J.,
RA Mclays S.H., Plumb R.W., Ramsay H., Ramsey Y., Rogers L., Ross M.T.,
RA Phillips S.H., Plumb R.W., Ramsay H., Ramsey Y., Rogers L., Ross M.T.,
RA Scott C.E., Sebra H.K., Skuce C.D., Smalley S., Smith M.L.,
RA Scott Und. C., Spragon L., Steward C.A., Sulston J.E., Swann R.M.,
Milliams L., Williams S.A., Williamson H., Willer T.E., Wilming L.,
RA Milliams L., Williams S.A., Williamson H., Wilmer T.E., Wilming L.,
Milliams L., Williams S.A., Williamson H., Wilmer T.E., Wilming L.,
RA Milliams L., Williams S.A., Williamson H., Wilmer T.E., Wilming L.,
RA Milliams L., Williams S.A., Williamson H., Wilmer T.E., Wilming L.,
RA Milliams J., Lewis S.L., In Williamson H., Wilmer T.E., Wilming L.,
RA Dorman A., Fang F., Fu Y., Hu P., Hua A., Kenton S., Lai H., Lao H.,
RA Dorman A., Fang F., Fu Y., Hu P., Hua A., Kenton S., Lai H., Lao H.,
RA Dorman A., Fang F., Fu Y., Hu P., Hua A., Kenton S., Lai H., Lao, Johnson D., Bemis G., Bentley D., Bradshaw H., Bourne S.,
RA Cordes M., Du Z., Fulton L., Goela D., Graves T., Hawkins J.,
RA Hinds K., Johnson D., Bemis G., Bentley D., Raterston R., Wilson D.,
RA Hinds K., Laylakh T., Kurahashi H., Saltta S., Budarf M., Kedra D.,
RA Mennel B.S., Shaikh T., Kurahashi H., Saltta S., Budarf M., Kedra D.,
RA Milkinson P., Bodentelch A., Hartman K., Khan A.S., Lane E.,
RA Milkinson P., Bodentelch A., Hartman K., Raber C. O'Srien K.,
RA Milkinson P., Bodentelch A., Hartman K.,
Raber B., Raber B., Rayla H., Rattman K.,
Raber B., Rayla H., Rayla H., Shingh 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-99397452; PubMed-10470851;
Kikuno R., Nagase T., Ishikawa K.-I., Hirosawa M., Miyajima N.,
Tanaka A., Kotani H., Nomura N., Ohara O.;
"Prediction of the coding sequences of unidentified human genes. XIV.
The complete sequences of 100 new cDNA clones from brain which code
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -- FUNCTION: Transcriptional repressor.
-- SUBCELLULAR LOCATION: Nuclear.
-- SUBCELLULAR LOCATION: Nuclear.
-- ALTERNATIVE PRODUCTS: 2 isoforms; 1 (shown here) and 2; are produced by alternative splicing.
-- TISSUE SPECIFICITY: Highest leavels in cerebellum.
-- SIMILARITY: BELONGS TO THE KRUEPPEL FAMILY OF C2H9-TYPE ZINC-FINGER PROTEINS. HIC TRANSCRIPTION FACTORS SUBFAMILY.
-- SIMILARITY: CONTAINS 1 BTB/FOZ DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Koehrer K., Beyer A., Mewes H.-W., Weil B., Wiemann S.; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases -: FUNCTION: Transcriptional repressor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "The DNA sequence of human chromosome 22.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   large proteins in vitro.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA Res. 6:197-205(1999).
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-; NOT\_ANNOTATED\_CDS.

EMBL;

EMBL; AJ313204; CAC70715.1; -. AF349035; AAK72951.1; -. AP000557; -; NOT\_ANNOTAT AB028943; BAA82972.1; -.

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Gaps
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0
                                                   pfam; pr00096; zf-C2H2; 5.
SMART; SMO0355; ZnF_C2H2; 5.
PROSITE; PS50097; BTB. 11.
PROSITE; PS50197; ZINC_FINGER_C2H2_1; 5.
PROSITE; PS50157; ZINC_FINGER_C2H2_2; 5.
Multigene family; Nuclear protein; Transcription regulation; DNA-binding; Zinc-finger; Metal-binding; Repressor;
                                                                                                                                                                                                                                                                                           DB 1; Length 615;
                                                                                                                                                                                                                                                                                                                  3; Indels
                                                                                                                                          DTB.
ZINC FINGERS.
C2H2-TYPE.
C2H2-TYPE.
C2H2-TYPE.
C2H2-TYPE.
C2H2-TYPE.
C2H2-TYPE.
MISSING TO CTBP.
MISSING TO CTBP.
IIM -> TIR (IN REF. 1).
Q -> R (IN REF. 4).
W; B0368C631B198C95 CRC64;
                                                                                                                                                                                                                                                                                                     Pred. No. 56;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                             Search completed: February 5, 2003, 09:48:19
Job time : 10.5714 secs
                                                                                                                                                                                                                                                                                            Score 45;
         Genew, HGNC:18595, HIC2.
InterPro; IPR000210; BTB_POZ.
InterPro; IPR000822; Znf_C2H2.
Pfam; PF00651; BTB; 1.
                                                                                                                                                                                                                                                                     66155 MW;
                                                                                                                                                                                                                                                                                           60.0%;
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les 7; Conservative
                                                                                                                                  Alternative splicing
                                                                                                                                                                                                                                                                                                                                                            386 GPYGEPPYPC 395
                                                                                                                                                                                                                                                                     615 AA;
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505
533
561
589
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CONFLICT
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VARSPLIC
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Title:
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Maximum DB seq length: 2000000000
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                Database :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Scoring table:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Run on:
SPTREMBL_21:*

1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_plage:*
10: sp_plant:*
11: sp_virus:*
12: sp_virus:*
13: sp_vertebrate:
14: sp_unclassifie
15: sp_bacteriap:*
17: sp_archeap:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     671580 seqs, 206047115 residues
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Gapop 10.0 , Gapext 0.5
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75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 ELGPQGRPPPPC 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
sp_vertebrate:*
sp_unclassified:*
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sp_bacteriap:*
sp_archeap:*
                                                                                                                                                                                          sp_invertebrate:*
sp_mammal:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

16	15	14	13	12	11	10	9	8	7	6	. <b>U</b> 1	4	· tu		. 1	Result No.
46	46	47	47	47	47	47	48	48	48	48	49	49	50	5	51	Score
61.3	61.3	62.7	62.7	62.7	62.7	62.7	64.0	64.0	64.0	64.0	65.3	65.3	66.7	68.0	68.0	Query Match
139	112	1827	635	333	329	67	1616	373	327	211	2241	858	411	297	261	Length
11	17	13	12	16	12	11	4	4	σ	S	υı	13	16	11	10	DB
Q9CTN9	Q9YEB0	Q8UUM5	Q69087	Q9L009	009798	Q9Z1I8	015054	Q9NP08	001799	045098	015850	Q8UVX0	Q9FCM3	Q9JLV7	Q9CAE4	Π
_	$\overline{}$	G	Q69087 human herpe	Q91009 streptomyce		Q9z1i8 rattus norv		Q9np08 homo sapien	001799 caenorhabdi	045098 caenorhabdi	O15850 leishmania	O	Q9fcm3 streptomyce	Q9jlv7 mus musculu	Q9cae4 arabidopsis	Description

45	44	43	42	41	40	39	38	37	36 6	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17
44	44	44	44	44	44	44	44	44	44	45	45	45	45	45	45	45	45	45	45	45	46	46	46	46	46	46	46	46
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329	309	297	243	238	176	173	142	142	85	1820	1184	756	705	533	533	432	388	363	363	253	1784	1500	1014	993	. 579	502	373	230
U	4	4	Ν	4	10	4	11	11	11	13	ഗ	16	4	10	10	ហ	4	10	10	G	10	10	G	ഗ	10	10	G	5
Q17166	Q04118	Q16038	Q9F1Q4	000600	Q9C4Z8	Q15214	Q8R5H4	Q8VCS6	070555	Q9I907	Q9V5D2	P72877	Q8TEJ5	Q9STK1	Q8VYS5	Q21414	Q96Н72	Q94C63	Q9ZU66	Q9VMF9	Q8S5L6	Q94DA0	Q9ВІЗ2	Q9VY31	Q9LGG8	Q8S5L3	Q9в131	Q9W3V7
brug	homo	┰.	ther	<del></del>	$\overline{}$	Q15214 homo sapien	mus	mus	070555 mus musculu	~	drosophila	P72877 synechocyst		arabidopsi	S		5	arabidopsi		drosophila	oryza	Q94da0 oryza sativ	Q9bi32 caenorhabdi	rosop	oryza sat	Q8s5l3 oryza sativ	caenorhab	Q9w3v7 drosophila

## ALIGNMENTS

RPO	RESULT Q9CAE4 AC Q AC Q DT 0 DT 0 DT 0 DT 0 C C C C C C C C C C C C C C C C C C C
SEQUENCE FROM N.A. SEQUENCE FROM N.A. SEQUENCE FROM N.A. STRAIN-CV. COLUMBIA; MEDLINE-21016720; PU SALABOUDAT M., LEMCK FARTMANN B., Valle G Delseny M., Boutry M. De Simone V., Chaisn Wincker P., Cattolic Schaefer M., Mueller Wirmbach E., Drzonek Wiedelmann R., Kranz Vezzi A., D'Angelo M. Conrad A., Hornische Reichelt J., Scharfe Ravarro P., Collado COOKE R., Laudie M., de Haan M., Maarse A Monfort A., Argiriou Mannhaupt G., Haase Mayer K.F. X., Kaul S Rooney T.H., Haas B. Pai G., Militscher J Preuss D., Lin X., N	LT 1  E4  Q9CAE4  Q9CAE4;  O1-JUN-2001 (TrE  O1-JUN-2002 (TrE  O1-JUN-2002 (TrE  F13M14.33
SEQUENCE FROM N.A. SETRAINE-CY, COLUMBIA; MEDILINE-21016720; Pubmed=11130713; Salanoubat M., Lemcke K., Rieger M., Fartmann B., Valle G., Bloecker H., F Delseny M., Boutry M., Grivell L.A., De Simone V., Choisne N., Artiquenave Wincker P., Cattolico L., Weissenbach Schaefer M., Mueller-Auer S., Gabel C. Wurmbach E., Drzonek H., Erfle H., JC Wiedelmann R., Kranz H., Voss H., Hol Vezzi A., D'Angelo M., Pallavicini A., COnrad A., Hornischer K., Kauer G., I Reichelt J., Scharfe M., Schoen O., E Navarro P., Collado C., Perez-Perez A. COOKE R., Laudie M., Berger-Llauro C. de Haan M., Maarse A.C., Alcaraz JF Monfort A., Argiriou A., Flores M., II Mannhaupt G., Haase D., Schoof H., Ko Mayver K.F. X., Kaul S., Town C.D., Ko Roconey T., Rizzo M., Walts A., Utterb Creasy T.H., Haas B., Maiti R., Wu D. Pai G., Militscher J., Sellers P., Gi Preuss D., Lin X., Nierman W.C., Salz	T 1  QCAE4 PRELIMINARY; PRT; 261 AA. QSCAE4; Q1-JUN-2001 (TrEMBLrel. 17, Created) Q1-JUN-2001 (TrEMBLrel. 17, Last sequence update) Q1-JUN-2002 (TrEMBLrel. 21, Last annotation update) Mypothetical 29.4 kDa protein. Hypothetical 29.4 kDa protein. F13M14.33. Arabidopsis thaliana (Mouse-ear cress). Arabidopsis thaliana (Mouse-ear cress). Eukaryota; Viridiplantae; Streptophyta; Embryophyta Spermatophyta; Magnoliophyta; eudicotyledons; core eurosids II; Brassicales; Brassicaceae; Arabidopsis MCBL_TaxID=3702;
Rieger M., Anso scker H., Perez vell L.A., Mach Artiguenave F., Weissenbach J., S., Gabel C., F S., Gabel C., F file H., Jordan lavicini A., Too Cauer G., Loehn Choen O., Bargu rez-perez A., O Calauro C., Pu Laraz JP. Co loaraz JP. Co loaraz JP. Co loaraz JP. Co loaraz JP. Co Laraz P., Gill J.	PRT; 261 , Created) , Last sequenc , Last annotat ein. e-ear cress). Streptophyta; ta; eudicotyle Brassicaceae;
rge W., Unseld -Alonso M., Ob e R., Puiddome Robert C., Br Saurin W., Qu uchs M., Benes N., Brandt P. ppo S., Simion ert TH., Nor es M., Terol J ttenwaelder B., Mas ottet A., Casa ri R., Vitale ri R., Vitale ri Zaccaria P.,	T 1  QCAE4 PRELIMINARY; PRT; 261 AA. QSCAE4; Q1-JUN-2001 (TrEMBLrel. 17, Created) O1-JUN-2001 (TrEMBLrel. 17, Last sequence update) O1-JUN-2002 (TrEMBLrel. 21, Last annotation update) O1-JUN-2002 (TrEMBLrel. 21, Last annotation update) Hypothetical 29.4 kDa protein. F13M14.33. Arabidopsis thaliana (Mouse-ear cress). Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis. MCBI_TaxID=3702;
M., ermaier B., nech P., ottier P., etier F., V., Nyakatura G., ati B., dsiek G., Climent J., Duchemin D., uy D., cuberta E., D., Mewes HW., Jenkins J., Shea T.P., Aken S., T.V., Venter J.C.,	Cheophyta; ots; Rosidae;

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MGD; MGI:1342772; K1f2.

InterPro; IPR0002965; P_rich_extensn.

InterPro; IPR000822; Znf_C2H2.

Pfam; PF00096; zf-C2H2; I.

PRINTS; PR01217; PRICHEXTENSN.

PRNITS; PR01217; PRICHEXTENSN.

SMART; SM00355; ZnF_C2H2; 1.

PROSITE; PS00028; ZINC_FINGER_C2H2_1; 1.

PROSITE; PS00028; ZINC_FINGER_C2H2_2; 1.

DNA-binding; Metal-binding; Zinc-finger.

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SEQUENCE 297 AA; 30812 MW; 4DF288DE1FF
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InterPro; IPRO01878; Znf_CCHC.
Pfam; PF00076; rrm; 1.
Pfam; PF00098; zf-CCHC; 1.
SMARP; SM00360; RRM; 1.
SMART; SM00343; ZnF_C2HC; 1.
PROSITE; PS50102; RRM; 1.
PROSITE; PS00039; RRM_RNP_1; UNKNOWN_1.
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01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last seq
01-JUN-2002 (TrEMBLrel. 21, Last anno
Lung kruppel-like factor (Fragment).
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EMBL; AC011560; AAG51392.1;
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
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SEQUENCE 2
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"Characterization of the lung Kruppel-like transcription
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72.7%;
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O9FCM3;
01-MAR-2001 (TrEMBLrel. 1
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Bacteria; Firmicutes; Actinobacteria; Actinobacterida
Bacteria; Firmicutes; Streptomycineae; Streptomycetaceae;
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"A set of ordered cosmids and a detailed genetic a
the 8 Mb Streptomyces coelicolor A3(2) chromosome.
Mol. Microbiol. 21:77-96(1996).
[4]
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Bentley S.D., Parkhill J., I
Submitted (AUG-2000) to the
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InterPro; IPR003042; Rng_mnoxygenase.
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Redenbach M., Kieser H.M., Denapaite D.,
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Brachydanio rerio (Zebrafish) (Zebra danio).

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01-JUN-1998
01-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wyler P.J., Audleman L., devos T., Hixson G., Kiser P Magness C., Rickel E., Sisk E., Sunkin S., Swartzell Bastien P., Fu G., Ivens A., Stuart K.;

"Leishmania major Friedlin chromosome 1 has an unusua protein coding genes.";

Proc. Natl. Acad. Sci. U.S.A. 96:2902-2906(1999).

EMBL; AE001774; AAC24680.1;
InterPro; IPR000008; C2.
InterPro; IPR0000937; Viral_coat.
                                                                                                                                                                                                             1855
    Hypothetical
                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                   PRINTS; PR00233; ICOSAHEDRAL.
SMART; SM00239; C2; 1.
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NCBI_TaxID=5664;
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01-NOV-1998
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"Cloning and characterization of zebrafish homolog of pi
for germ-line stem cell self-renewal.";
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF33369; AAL57170.1; -.
InterPro; IPR003109; PAZ.
InterPro; IPR003165; Piwi.
Pfam; PF02170; PAZ; 1.
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NCBI_TaxID=7955;
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(TTEMBLrel. 06, Created)
(TTEMBLrel. 06, Last sequence update)
(TTEMBLrel. 21, Last annotation update)
L 24.1 kDa protein.
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A; 241669 MW;
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88.9%;
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77.8%;
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Hypothetical
F53G12.7.
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Hypothetical protein.
SECHENCE 211 AA; 2
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STRAIN-BRISTOL N2;
Bentley D., Le T.T.;
Bendley Of C. elegans (
                                          STRAIN-BRISTOL Waterston R.;
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STRAIN=BRISTOL N2;
MEDLINE=99069613; PubMed=9851916;
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Rhabditidae; Pelode;
NCBI_TaxID=6239;
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                      Waterston R.;
"Direct Submission ";
                                                                 SEQUENCE FROM N.A. STRAIN-BRISTOL N2;
                                                                                                                                  Submitted
                                                                                                                                                                                                                                                            "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium. Science 282:2012-2018(1998).
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MEDLINE=99069613; PubMed=9851916;
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Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
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Peloderinae; Caenorhabditis.
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EMBL/GenBank/DDBJ databases.
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InterPro; IPR000087; Collagen.
InterPro; IPR002486; Co__cuticle_N.
Pfam; PF01391; Collagen; 2.
Pfam; PF01484; Col_cuticle_N; 1.
ProDom; PD000007; Collagen; 1.
ProDom; PD000007; Collagen; 1.
Hypothetical protein.
SEQUENCE 327 AA; 33025 MW; 1DFACE
                                   O15054; PRELIMINARY;
O15054; PRELIMINARY;
O1-JAN-1998 (TrEMBLrel. 05,
O1-JAN-1998 (TrEMBLrel. 05,
O1-JUN-2002 (TrEMBLrel. 21,
                                                                                                                                                                                                                                                                                                                                                                                                                        -!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY). EMBL; M99587; AAF70205.1; -. HSSP; P14653; 1B72.
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MEDLINB-93087572; PubMed-1360670;
Stadler H.S., Padanilam B.J., Buetow K., Murray J.C
"Identification and genetic mapping of a homeobox go
region of human chromosome 4.";
Proc. Natl. Acad. Sci. U.S.A. 89:11579-11583(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                 PRINTS; PRO0024; HOMEOBOX.
PRINTS; PRO0031; HTHREPRESSR.
ProDom; PD000010; Homeobox; 1.
SMART; SM00389; HOX; 1.
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            KIAA0346 protein (Fragment) KIAA0346.
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SEQUENCE 373 AA; 39225 MW; 8BF9EB1722660A76 CRC64;
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InterPro; IPR000047; HTH_repressr.
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sapiens (Human).
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7; Conserv
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8; Conserv
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72.7%;
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Pred. No. 13;
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Q9Z118
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Matches 7
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DNA Res. 4:141-150/1007
                                                                                                                                                                                                                                                                                                                                                                                                              Q92118;
Q92118;
Q1-MAY-1999 (TrEMBLrel. 10,
Q1-MAY-1999 (TrEMBLrel. 10,
Q1-JUN-2001 (TrEMBLrel. 17,
O09798 PRELIMINARY;
O09798;
O1-JUL-1997 (TrEMBLrel.
O1-JUL-1997 (TrEMBLrel.
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SEQUENCE
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                                                                                                                                                                                                  "Isolation and characterization of t
Biochem. J. 336:227-234(1998).
EMBL; AJ224997; CAA12281.1; -
InterPro; IPR002965; P. rich_extensn.
PRINTS; PR01217; PRICHEXTENSN.
                                                                                                                                                                                                                                                                                                                                                       Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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                                                                                                                                                                                                                                                                                                                                                                                                      Huntingtin (Fragment).
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PRINTS; PR01217; PRICHEXTENSN.
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InterPro; IPR003347; TF_JmjC.
InterPro; IPR001440; TPR.
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wa K., Nakajima
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70.0%;
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87.5%;
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Pred. No. 56;
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l; Mismatches
                                                                                                                                                                Score 47;
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Sciurognathi; Muridae;
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                                                                                                                                                                                                                                                             rat Huntingtin promoter.";
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RESULT Q91009
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Q9L009;
Q1-QT-2000 (TrEMBLrel. 15, Created)
Q1-QT-2000 (TrEMBLrel. 15, Last sequence update)
Q1-UN-2002 (TrEMBLrel. 21, Last annotation update)
Putative dehydrogenase.
SCO2304 OR SCC30.12C.
Streptomyces coelicolor.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; St
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human herpesvirus 1.
"'rnses; dsDNA viruses, no RNA su
"'rnses; Simplexvirus.
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Nucleic Acids Res. 14:1727-1745(1986).
  STRAIN=A3(2);
Seeger K.J.,
                                          SEQUENCE FROM N.A.
                                                                                   NCBI_TaxID=1902;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00716; SEQUENCE 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted
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Dolan A., McKie E.
"Status of the ICF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=86148504; PubMed=3005980; McGeoch D.J., Dolan A., Donald S., Brauer D.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-88274327; PubMed=2839594;
MCGeoch D.J., Dalrymple M.A., Davison A.J., Dolan A.,
MCMab D., Perry L.J., Scott J.E., Taylor P.;
"The complete DNA sequence of the long unique region herpes simplex virus type 1.";
J. Gen. Virol. 69:1531-1574(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              McGeoch D.J.;
Submitted (JAN-1989)
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Harris
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      80; PubMed=1321882;
e E., MacLean A.R., McGeoch D.J.
ICP34.5 gene in herpes simplex
                                                                                                       Streptomycineae;
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Q69087;
01-NOV-1996
01-NOV-1996
01-DEC-2001
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BentLey S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins i
Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth
Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S
        SEQUENCE
                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. MEDLINE=94308117; Darke P.L., Chen E
                                                                                                                                                                         J. Biol. Chem. EMBL; L32018;
                                                                                                                                                                                                                                                                                                                                                                            Viruses; dsDNA viruses,
Alphaherpesvirinae; Simp
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Nature 417:141-147(2002).
EMBL; AL352972; CAB88182.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rabbinowitsch E., Rajandream M.A., Rutherford K., Rutter S., Seeger K., Saunders D., Sharp S., Squares R., Squares S., Tawarren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "A set of ordered cosmids and a detaile
the 8 mb Streptomyces coelicolor A3(2)
Mol. Microbiol. 21:77-96(1996).
                                                                      PRINTS;
                                                                                                               InterPro;
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MEROPS; S21.001;
                                                                                                                                                                                                                  Escherichia coli."
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                                                                                                                                                                                                                                                                                                                                                                                                                         human herpesvirus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Redenbach M., Kieser H.M.
Kinashi H., Hopwood D.A.;
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Cerdeno A.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (APR-2000)
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                                                                                   Pro; IPR001847; Assemblin. PF00716; Peptidase_S21; 1.
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8; Conser
                                                                  PR00236; HSVCAPSIDP40.
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                              610
        66454 MW;
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e EMBL/GenBank/DDBJ databases.
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HSV-1 PROTEASE.
ICP35 ASSEMBLY PROTEIN.
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RESULT 15
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Q8UUMS
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Best Local Similarity
"~+~hes 7; Conserv?
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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pfam; pF01410; CCLF; 1.

pfam; pF0210; TSPN; 1.

pfam; pF02210; TSPN; 1.

proDom; pD002078; Fib_collagen_C; 1.

smarr; sm00208; CCLF; 1.

smarr; sm00282; LamG; 1.

smarr; sm00210; TSPN; 1.

pr0SITE; pS50025; LAM_G_DOMAIN; 1.

sequence 1827 AA; 181589 MW; AF
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01-MAR-2002
01-JUN-2002
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
Beloniformes; Adrianichthyldae; Oryzianae; Oryzias.
                                                                                                                                                                O9YEBO;
O1-NOV-1999 (TrEMBLrel. 12, Cr
O1-NOV-1999 (TrEMBLrel. 20, La
O1-MAR-2002 (TrEMBLrel. 20, La
Hypothetical protein APE0664.
                                                                                Aeropyrum pernix.
Archaea; Crenarchaeota; Thermoprotei;
Desulfurococcaceae; Aeropyrum.
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EMBL; AB073376; BAB83839.1; -.
EMBL; AB073376; Collagen.
InterPro; IPR000085; Fib_collagen_C.
InterPro; IPR001791; Laminin_G.
InterPro; IPR003129; TSPN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-HD-RR;
                                                                                                                                                                                                                                                                                                Q9YEB0
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STRAIN-K1;
                     SEQUENCE FROM N.A
                                                             NCBI_TaxID=56636;
                                                                                                                                                         APE0664.
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Pred. No.
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Pred. No. 88;
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AF5C71E9B38906EA CRC64;
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Kawarabayasi Y., Hino Y., Horikawa H., Yamazaki S., Haikawa Jin-no K., Takahashi M., Sekine M., Baba S.-I., Ankai A., K Jin-no K., Takahashi M., Sekine M., Baba S.-I., Ankai A., K Hosoyama A., Fukui S., Nagai Y., Nishijima K., Nakazawa H., Takamiya M., Masuda S., Funahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A., Aoki K.-I., Kubota K., Yamazaki J., Kushida N., Oguchi A., Aoki K.-I., Kubota K., Yakamura Y., Nomura N., Sako Y., Kikuchi H.; Toppitum sequence of an aerobic hyper-thermophilic crenarchaeon, Aeropyrum pernix Kl.";
DNA Res. 6.83-101(1999).
                                                                                                                                   EMBL; APRO00060; BAA79636.1; -.
Hypothetical protein; Complete proteome.
SEQUENCE 112 AA; 11931 MW; 9007CDD89321151E CRC64;
71
                                4 PQGRPPPPC 12
PQSRPPSPC 79
                                                                  Similarity 7; Conserv
                                                                    Conservative
                                                                                    61.3%;
77.8%;
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Pred. No. 9.
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                                                                                                    DB 17; Length 112;
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Search completed: February 5, 2003, 09:49:16
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Result
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Maximum DB
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Perfect score:
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       Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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1: /cgn2_6/ptodata/1

2: /cgn2_6/ptodata/1

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length: 2000000000
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US-08-257-273B-8
US-08-257-273B-8
US-08-98-257-2
US-09-798-267-2
US-09-798-267-3
US-09-798-267-3
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ALIGNMENTS

#### Query Match Best Local Similarity "-+~hes 9; Conserv ; MOLECULE TYPE: US-08-446-692-73 US-08-446-692-73 REFERENCE/DOCKET NUMBER: 1151 TELECOMMUNICATION INFORMATION: TELEPHONE: (212)415-8745 TELEPAX: (516)751-6849 INFORMATION: FOR SEQ ID NO: 73: SEQUENCE CHARACTERISTICS: LENGTH: 11 amino acids COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMPAILIBLE OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION DATA: APPLICATION UNMBER: US/08/446,692 FILING DATE: 7-JUN-1995 CLASSIFICATION: 424 Patent No. Sequence 73, Appl Patent No. 575955 GENERAL INFORMATION: ATTORNEY/AGENT INFORMATION: NAME: Maria C.H. Lin REGISTRATION NUMBER: 29,323 APPLICANT: Wang, Chang Yi APPLICANT: Zamb, Tinothy TITLE OF INVENTION: Inmunogenic LHRH peptide constructs TITLE OF INVENTION: and synthetic universal immune stimumber OF SEQUENCES: 114 CORRESPONDENCE ADDRESS TYPE: ami STREET: 345 Par CITY: New York STATE: NY COUNTRY: US ADDRESSEE: Maria C.H. Lin STREET: 345 Park Avenue amino acid GY: linear 10154-0053 Application Conservative peptide 74.7%; 81.8%; US/08446692 1 1151-4146 US2 Score 56; [ Pred. No. 0. Mismatches universal immune stimulators for vaccines DB 1; 0.077; Length 11; 0; Gaps 0,

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                                                                                                  Sequence 2, Application US/08188223 Patent No. 5688506
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Ladd, Anna | APPLICANT: Ladd, Anna | APPLICANT: Wang, Chang Yi APPLICANT: Zamb, Timothy Timothy Timothy Fine Province Chrr Peptide constructs TITLE OF INVENTION: Immunogenic LHRH peptide constructs TITLE OF INVENTION: and synthetic universal immune stimulators for vaccines NUMBER OF SEQUENCES: 114
CORRESPONDENCE ADDRESS:
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NAME: Maria C.H. Lin
REGISTRATION NUMBER: 29,
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    APPLICANT: Grimes, Stephen
APPLICANT: Scibienski Robert
TITLE OF INVENTION: Immunogens
TITLE OF INVENTION: Releasing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/446,692
FILING DATE: 7-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: peptide
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APPLICATION NUMBER: US 08/229,275
FILING DATE: 14-APR-1994
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REFERENCE/DOCKET NUMBER: 1151-4146
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Local Similarity 81.8%;
les 9; Conservative
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345 Park Avenue
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(516)751-6849
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Immunogens Against
Releasing Hormone
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Pred. No. 0.077;
                Against Gonadotropin
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US-08-968-466-2
; Sequence 2, Application US/08968466
; Patent No. 6132720
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TELEPAX: 212-354-8113
TELEFAX: 212-354-8113
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
'ENGTH: 16 amino acids
                                                                                                                                                                                                            GENERAL INFORMATION:
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/188,223
FILING DATE: 27-JAN-1994
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                       APPLICANT: Grimes, Stephen APPLICANT: Scibienski, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
COMPUTER READABLE FORM:
                                                                                                             NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                           TITLE OF INVENTION: Immunogens Against TITLE OF INVENTION: Releasing Hormone
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STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: OTHER INFORMATION:
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                            COUNTRY:
                                                              STREET: 1155 Av. CITY: New York
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STREET: 1155
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SYSTEM: PC-DOS/MS-DOS
                                                                             Dimitrios T. Drivas, Esq
55 Avenue of the Americas
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/note= "pyroglutamic acid (5-oxoproline)"
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                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
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                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOGTWARE: Patentin Release #1.0, Version #1.25
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NAME/KEY: Region
LOCATION: 1..10
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LENGTH: 16 amino acids
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                               CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/0:
FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: TITLE OF INVENTION: NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                APPLICANT: Grimes, Stephen APPLICANT: Scibienski, Rob
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LOCATION: 11..16
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Drivas Esq., Dimitrios T. REGISTRATION NUMBER: 32,218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/0 FILING DATE: 27-JAN-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC OPERATING SYSTEM:
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REFERENCE/DOCKET NUMBER: 1102865-300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10 GRPPPPC 16
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CLASSIFICATION: 424
IOR APPLICATION DATA:
                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                            STATE:
                                                                                                                                                                                                                           CITY: New York
                                                                                                                                                                                                                                             STREET:
                                                                                                                                                                                                                                             ADDRESSEE: Dimitrios T. Drivas, Esq. STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION:
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                                                                                                                                                                        RY: USA
10036-2787
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YES
                                                                                                                                                                                                                                                                                                               Tumors with Immunogens against Gonadotropin Releasing Hormone
                                                                                                                                                                                                                                                                                                                                   Methods for the Treatment of Hormone-Dependent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                64.0%; Score 48; DB 4; Length 16; 100.0%; Pred. No. 1.2;
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/note= "pyroglutamic acid (5-oxoproline)"
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                                                 US/08/478,546B
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RESULT 6
US-07-832-855-2
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                       APPLICANT: ROIZHMAH, LOL.
APPLICANT: Liu, Fenyong
TITLE OF INVENTION: Methods and Compositions of a
TITLE OF INVENTION: Preparation and Use of A Herpe
TITLE OF SPOHENCES: 15
                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
                                                                                                                                        SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
                                                            ATTORNEY/AGENT INFORMATION: NAME: Coolley, Ronald B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: peptide
              TELECOMMUNICATION INFORMATION:
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                             REGISTRATION NUMBER: 27,187
REFERENCE/DOCKET NUMBER: ARCD045
                                                                                           FILING DATE: 1: CLASSIFICATION:
                                                                                                                          APPLICATION NUMBER:
                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                 STATE:
                                                                                                                                                                                                                                                                                 CITY: Chicago
                                                                                                                                                                                                                                                                                             ADDRESSEE: ARNOLD, WHITE & DURKEE
STREET: 321 No. 5478727th Clark Street, Suite 800
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 TELEPHONE:
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Pred. No.
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RESULT 8
US-08-457-273B-8
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US-08-176-320-2
                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/705
FIGURG DATE: 24 MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: COOLEY, Ronald B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312)744-0090
INFORMATION FOR SEQ ID NO: 2:1
Sequence 8, Application Patent No. 5849995 GENERAL INFORMATION: APPLICANT: Hayden, M
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Best Local S
Matches 7
                                                                                                                                                                                    Matches
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATIBLE
COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/176,320
                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 635 amino acids
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CORRESPONDENCE ADDRESS: Alice O. Martin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Liu, Fenyong
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE
TITLE OF INVENTION: PREPARATION AND USE OF A HERPES !
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                                                                                                                       565 PPGPPPPPC 573
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STRANDEDNESS: sir
TOPOLOGY: linear
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nes 7; Conserv
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77.8%;
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Pred. No.
                                                                                                                                                                                               Score 47; DE
Pred. No. 54;
                                                                                                                                                                                Mismatches
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US-08-246-982A-16
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            COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1

CURRENT APPLICATION DATA:

CURRENT APPLICATION NUMBER: US/08/246,982A
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Best Local S
Matches 7
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Patent No. 5
                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                     APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS:
TOPOLOGY: line
MOLECULE TYPE: 1
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TELEPHONE: 919-854-1400
TELEFAX: 919-854-1401
                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
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MEDIUM TYPE: Floppy disk
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Virginia Bennett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                  TITLE OF INVENTION: Huntingtin DNA, Protein And Uses Thereof NUMBER OF SEQUENCES: 25
                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION: NAME: Bennett, Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: Mouse model for Huntington's Disease TITLE OF INVENTION: Related DNA Sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
APPLICATION NUMBER: (FILING DATE: May 20, CLASSIFICATION: 435
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STRRET: PO DO...
CITY: Raleigh
CTTMRE: No. 5849995th Carolina
                                                                                                                                                                                               STREET: 1100 New CITY: Washington
                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          45 PQGQPPPP 52
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                                                                                                                                                                                      STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Bennett, Virginia REGISTRATION NUMBER: 37, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: FILING DATE: CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC
OPERATING SYSTEM:
                                                                                                                                                                                                                                     ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 PQGRPPPP 11
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                                                                                                                                                                                                                                                                                                                                                                                          5, Application US/08246982A 5686288
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                                                                                                                                                                                  D.C.
                                                                                                                                                                                                                   E: Sterne, Kessler, Goldstein & Fox 1100 New York Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3118 amino acids
                                                                                                                                                                                                                                                                                                   Gusella, James F.
                                                                                                                                                                   U.S.A.
                                                                                                                                                                                                                                                                                                                                                       MacDonald, Marcy E
                                                                                                                                                                                                                                                                                                                     Ambrose, Christ
Duyao, Mabel P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lin, Biaoyang
Nasir, Jamal
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SYSTEM: PC-DOS/MS-DOS
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87.5%;
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Pred. No. 2.4e+02;
1; Mismatches 0
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                                                                 #1.25
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; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: prot
US-08-453-265-16
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                                                             Matches
                                                                             Query Match
Best Local
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                                                                                                                                                                                                                TELEFAX: (202) 371-2540 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                           CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: LUGWIG, Steven R.
REGISTRATION NUMBER: 36,203
REFERENCE/DOCKET NUMBER: 0609
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
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APPLICANT: Duyao, Mabel P.
APPLICANT: Gusella, James F.
TITLE OF INVENTION: Huntingtin DNA, Protein And Uses Thereof
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: GOLÓSTEIN, JOTGE, A.
REGISTRATION NUMBER: 29,021
REFERENCE/DOCKET NUMBER: 06:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 3119 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: MacDonald, Marcy E. APPLICANT: Ambrose, Christine M.
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 45
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les 7; Conserv
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                                                           Local Similarity es 7; Conserv
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                              4 PQGRPPPP 11
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PQGQPPPP 52
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5693757
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87.5%;
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                                                                        Score 47;
Pred. No.
                                                          Mismatches
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ches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2, Application US/08237919
Patent No. 5610281
GENERAL INFORMATION:
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Best Local Similarity 72.7%;
Matches 8; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                        TITLE OF INVENTION: Methods and Compositions for Modulating Heterotypic TITLE OF INVENTION: E-cadherin Interactions with T Lymphocytes NUMBER OF SEQUENCES: 8
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NAME: Plumer, Elizabeth R
REGISTRATION NUMBER: 36,6
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/237,919
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: Wolf, Greenfield & Sacks P.C
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ADDRESSEE: Wolf, Gre
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                                                                                                                                                                                                                                                                                      APPLICANT:
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STREET: BOSton
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TOPOLOGY:
                                                                                                                                STATE: MA
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CLASSIFICATION: 424
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ZIP: 02210
                                                                                               ZIP: 02210
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   SOFTWARE:
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                                                                                                                                                                 600 Atlantic Avenue
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PatentIn Release #1.0, Version #1.25
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CURRENT APPLICATION DATA:

APPLICATION NUMBER:

US/08/732,429

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RESULT 14
US-09-798-267-3
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Best Local Similarity
Thes 8; Conserve
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                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PRINCE SEQ ID NO 2
LENGTH: 878
                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sequence 2, Application US/09798267 Patent No. 6406870
                                                                    Sequence 3, Application US, Patent No. 6406870
                                                                                                                                                                                                                                                  Query Match
Best Local :
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      APPLICANT: Brenner, Micl
APPLICANT: Cepek, Karyn
TITLE OF INVENTION: Me
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Brenner, Michael
APPLICANT: Cepek, Karyn
TITLE OF INVENTION: Methods and Compositions for Modulating Heterotypic E-cadherin
TITLE OF INVENTION: Interactions with T Lymphocytes
FILE REFERENCE: L0560/7008ERP
CURRENT APPLICATION NUMBER: US/09/798,267
CURRENT FILING DATE: 2001-03-02
                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: PCT, PRIOR FILING DATE: 195-05-03 PRIOR APPLICATION NUMBER: US 0 PRIOR FILING DATE: 1996-11-01
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INFORMATION FOR SEQ ID NO: 2:
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APPLICATION NUMBER: 08/2:
FILING DATE: 3 May 1994
ATTORNEY/AGENT INFORMATION:
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TELEPHONE: 617-720-3500
TELEFAX: 617-720-2441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS: LENGTH: 878 amino acids
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nes 8; Conserv
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                                    Brenner, Micha
                                                                                                                                                                                                                                   Conservative
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Methods and Compositions for Modulating Heterotypic E-cadherin
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72.7%;
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72.7%;
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Pred. No.
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Pred. No.
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Mismatches
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Best Local Similarity
*** 8; Conserva
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                                                                PCT-US95-05518-2
Query Match
Best Local Similarity
Matches 8; Conserv
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SEQ ID NO 3
                                                                                                                                         INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER:
PRIOR FILING DATE: 1996-
NUMBER OF SEQ ID NOS: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/798,267
CURRENT FILING DATE: 2001-03-02
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TYPE: PRT
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PRIOR FILING DATE: 1995-05-03
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: FILE REFERENCE: LC
                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                              FILING DATE: herewith PRIOR APPLICATION DATA: APPLICATION NUMBER: 08/2: FILING DATE: 3 May 1994 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Rel CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: Wolf, Greenfield & Sacks P.C
                                                                          TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                      TELECOMMUNICATION INFORMATION: TELEPHONE: 617-720-3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
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                                                                                                              TYPE:
                                                                                                                                                                           TELEFAX:
                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                    NAME: Plumer, Elizabeth R REGISTRATION NUMBER: 36,6
                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: MA
                                                                                                                         LENGTH:
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1996-11-01
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1994-05-03
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                Score 46;
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Search completed: February 5, 2003, 09:50:19
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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         Published_Applications_AA:*

1: /cgn2_6/ptodata/2/pubpaa/U
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3: /cgn2_6/ptodata/2/pubpaa/U
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length: 2000000000
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/cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
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/cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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US-09-788-657-23	US-09-764-864-1261	US-09-764-864-800	US-09-957-995A-10	US-10-192-257-1	US-10-192-257-3	US-10-192-257-5	US-09-894-998-3	US-09-850-887-4	US-09-964-899-33	US-09-823-038A-33	US-10-001-887-137	US-09-905-831-21	US-09-919-497-56	US-10-001-887-108	US-09-905-983-48	US-10-165-049-3	US-10-165-049-2	US-10-192-257-2	ID
Sequence 23, Appl	Sequence 1261, Ap	80	10	1		D		4	Sequence 33, Appl	Sequence 33, Appl	137,	`	Sequence 56, Appl	Sequence 108, App	e 48		Sequence 2, Appli	Sequence 2, Appli	Description

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US-09-193-663-4	US-10-017-910-5	US-08-971-317A-4	US-09-899-059-6	US-09-246-129B-6	us-09-770-906-2	US-09-925-301-1078	US-09-764-887-279	US-09-867-550-1410	US-09-864-761-43362	US-09-780-996-7	US-09-925-300-962	US-09-738-973-425	US-09-854-133-425	US-09-785-770A-16	US-09-785-770A-17	US-09-904-065-19	US-09-904-065-18	US-09-904-065-17	US-09-904-065-16	US-09-904-065-10	US-09-904-065-8	US-09-904-065-6	US-09-957-995A-19	US-09-823-240-2	US-U9-925-300-1444
e 4,	ر د	4		Sequence 6, Appli		1078,	279,			Sequence 7, Appli	Sequence 962, App	Sequence 425, App	425,	16,		19,	Sequence 18, Appl	17,	16,	10	8	6			Sequence 1444, Ap

#### ALIGNMENTS

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                                                                                                                                  RESULT 2
US-10-165-049-2
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US-10-192-257-2
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Best Local Similarity 80...
Shown the Best Local Similarity 80...
                                                                       Sequence 2, Application US/10165049 Publication No. US20020192724A1 GENERAL INFORMATION:
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Publication No. US20030021786A1
GENERAL INFORMATION:
APPLICANT: Aphton Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
APPLICANT: Brenner, Michael
APPLICANT: Cepek, Karyn
TITLE OF INVENTION: Methods and Compositions for Modulating Heterotypic E-cadherin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: Treatment and Prevention of Cancerous and Pre-Cancerous Condit
TITLE OF INVENTION: Liver, Lung and Esophagus
FILE REFERENCE: 1102865-0057
CURRENT APPLICATION NUMBER: US/10/192,257
CURRENT FILING DATE: 2002-07-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT FILING DATE: 2002-07-09
PRIOR APPLICATION NUMBER: US 60/303,868
PRIOR FILING DATE: 2001-07-09
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PRIOR FILING DATE: 1994-05-03
PRIOR APPLICATION NUMBER: PCT/US 95/05518
PRIOR FILING DATE: 1995-05-03
PRIOR APPLICATION NUMBER: USSN 08/732,429
PRIOR APPLICATION NUMBER: USSN 08/732,429
PRIOR FILING DATE: 1996-11-01
PRIOR APPLICATION NUMBER: USSN 09/798,267
PRIOR FILING DATE: 2001-03-01
NUMBER OF SEQ ID NOS: 9
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SEQ ID NO 2
LENGTH: 878
TYPE: PRT
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Best Local
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SEQ ID NO 3
LENGTH: 878
TYPE: PRT
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PRIOR APPLICATION NUMBER: PCT/US 95/05518
PRIOR FILING DATE: 1995-05-03
PRIOR APPLICATION NUMBER: USSN 08/732,429
PRIOR FILING DATE: 1996-11-01
PRIOR APPLICATION NUMBER: USSN 09/198,267
PRIOR FILING DATE: 2001-03-01
                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: Methods and Compositions for Modulating Heterotypic E-cadherin TITLE OF INVENTION: Interactions with T Lymphocytes FILE REFERENCE: L00560/70010ERP CURRENT APPLICATION NUMBER: US/10/165,049 CURRENT FILING DATE: 2002-06-07 PRIOR APPLICATION NUMBER: USN 08/237,919
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CURRENT FILING DATE: 2002-06-07
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LOCATION: (2225)..(2295)
OTHER INFORMATION: transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: misc_feature LOCATION: (800)...(808) OTHER_INFORMATION: HAV tripeptide
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Pred. No. 96;
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Whiches 8; Conserve
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                                                                                         RESULT 6
US-09-919-497-56
                                                                                                                                                                                                                                                                                                                   ; TYPE: PRT; ORGANISM: Homo sapien US-10-001-887-108
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APPLICANT: Gelger, Benjamin
APPLICANT: Ben-Ze'ev, Avri
APPLICANT: Ben-Ze'ev, Avri
APPLICANT: Sadot, Einat
TITLE OF INVENTION: METHODS AND THERAPEUTIC COMPOSITIONS FOR TREATING CANCER
                                  Sequence 56, Application U Patent No. US20020106662A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Salceda, s
APPLICANT: Macina, r
APPLICANT: Recipon,
APPLICANT: Cafferkey
APPLICANT: Sun, Yong
APPLICANT: Liu, Cher
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 48, Application US/09905983 Patent No. US20020045591A1
                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO 108
LENGTH: 638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 108, Application US/10001887 Patent No. US20020155464A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILE REFERENCE: 01/23326
CURRENT APPLICATION NUMBER: US/09/905,983
CURRENT FILING DATE: 2001-09-28
NUMBER OF SEQ ID NOS: 60
APPLICANT: Mutter, George L.
TITLE OF INVENTION: PROGNOSTIC CLASSIFICATION OF ENDOMETRIAL CANCER
                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/10/001,887
CURRENT FILING DATE: 2001-11-20
PRIOR APPLICATION NUMBER: 60/249,998
PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: 60/252,563
PRIOR FILING DATE: 2000-11-22
NUMBER OF SEQ ID NOS: 137
                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: Compositions and Methods Relating to Breast Specific Genes FILE REFERENCE: DEX-0269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ENGTH: 878
                                                                                                                                                                     124 EPGPQGEPGPP 134
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Sun, Yongming
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                                                                       Application US/09919497
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72.7%;
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Pred. No.
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Pred. No.
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US-10-001-887-137
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                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 21
LENGTH: 34
TYPE: PRT
               GENERAL INFORMATION: APPLICANT: Salceda, APPLICANT: Macina,
                                                                                                                                                                                                                               Best Loc
Matches
                                                               Sequence 137, Application US/10001887 Patent No. US20020155464A1
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Patent No. US20020119572A1
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Hamad, Kimberly APPLICANT: Zhang, Shuguang TITLE OF INVENTION: Direct, FILE REFERENCE: MLB-086
                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: US 60/218,312
PRIOR FILING DATE: 2000-07-14 
NUMBER OF SEQ ID NOS: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Jacobson, Joseph
APPLICANT: Schwartz, John
APPLICANT: Hamad, Kimberly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILE REFERENCE: B0801/7225
CURRENT APPLICATION NUMBER: US/09/919,497
CURRENT FILING DATE: 2001-07-31
PRIOR APPLICATION NUMBER: US 60/221,735
PRIOR FILING DATE: 2000-07-31
NUMBER OF SEQ ID NOS: 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/905,831
CURRENT FILING DATE: 2001-07-13
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: US 60/276,313 PRIOR FILING DATE: 2001-03-16
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NAME/KEY: UNSURE
LOCATION: (758)...(758)
OTHER INFORMATION: Xaa
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                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: PXY34 peptide
                                                                                                                                                                                                                                                                                                                                 FEATURE:
                                                                                                                                                                                                                                                                                                                                               ORGANISM: Artificial Sequence
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Recipon, Herve
             Macina, Roberto
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Pred. No. 2.5e+02;
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8.5;
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Best Local Similarity
Them 7; Conserv
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                                                                                                                                 ; Patent No. US20020174446A1 ; GENERAL INFORMATION:
                                                                                                                                                                                      US-09-964-899-33
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APPLICANT: Strachan, Lorna
APPLICANT: Sleeman, Matthew
APPLICANT: Aleeman, Matthew
APPLICANT: Onrust, Rene
APPLICANT: Onrust, Rene
APPLICANT: Murison, Greg
TITLE OF INVENTION: Compositions Isolated From Stromal Cells
FILE REFERENCE: 11000.1037c3
                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/823,038A CURRENT FILING DATE: 2001-07-09 NUMBER OF SEO ID NOS: 61
SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 33
LENGTH: 322
TYPE: PRT
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SOFTWARE: PatentIn version 3.1
SEQ ID NO 137
                                                                                                                                                                       Sequence 33,
                                                                                                                                                                                                                                                                                                                                      Matches
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Best Local
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APPLICANT: Cohen, Dalia et al.

TITLE OF INVENTION: Identification of Genes Involved in
TITLE OF INVENTION: Alzheimer's Disease Using Drosophila Melanogaster
FILE REFERENCE: 4-31612 A -31612 A CURRENT APPLICATION NUMBER: US/09/964,899
CURRENT FILING DATE: 2001-09-27
PRIOR APPLICATION NUMBER: 60/236,893
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CURRENT APPLICATION NUMBER: US/10/001,887

CURRENT FILING DATE: 2001-11-20

PRIOR APPLICATION NUMBER: 60/249,998

PRIOR FILING DATE: 2000-11-20

PRIOR APPLICATION NUMBER: 60/252,563

PRIOR FILING DATE: 2000-11-22
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APPLICANT: Liu, Chenghua
TITLE OF INVENTION: Compositions and Methods Relating to Breast Specific Genes and
                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Human
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                                                                                                                                                                       Application US/09964899
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77.8%;
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Pred. No.
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Pred. No.
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67;
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13;
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NUMBER OF SEQ ID NOS: 53
SOFTWARE: FastSEQ for Windows Version 4.0

PRIOR FILING DATE: 2000-09-29
PRIOR APPLICATION NUMBER: 60/
PRIOR FILING DATE: 2001-06-14

60/298,309

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US-09-850-887-4
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LENGTH: 1249
TYPE: PRT
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Patent No. US20020009778A1
GENERAL INFORMATION:
APPLICANT: Lal, Preeti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 63.6%; Matches 7; Conservative
                                                                                Matches
                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: CERRONE, MICHAEL C.
REGISTRATION NUMBER: 39,132
REFERENCE/DOKET NUMBER: PF-0535
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEPHONE: (650) 845-4166
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             839 EIPPRRRPPPP 849
                                                                                Local Similarity
nes 7; Conserv
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        3 GPQGRPPP 10
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FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPDATIBLE
COMPUTER: Floppy disk
COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/09/850,887
FILING DATE: 07-May-2001
CLASSIFICATION: -CURKNOWN>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GOIGONE, GINA
TITLE OF INVENTION: THYROID AND PITUITARY MEMBRANE PROTEIN
NUMBER OF SEQUENCES: 4
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ADDRESSEE: INCYTE PHARMACEUTICALS, INC
                                                                                                                                                                                                                                                                             SEQUENCE DESCRIPTION: SEQ ID NO: 4 :
                                                                                                                                                                                                                                                                                                                                                                                              IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                      LIBRARY: GenBank CLONE: g206712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 274 amino acids
TYPE: amino acid
STRANDEDNESS: single
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STATE: CALIFORNIA
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                                                                                Conservative
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                                                                                                                    57.3%;
87.5%;
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Pred. No. 2.3e+02;
                                                                                                                    Score 43; DB Pred. No. 77;
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Query Match
Best Local Similarity
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                                                                                                                                       ; OTHER INFORMATION: Hypothetical spacer peptide US-10-192-257-5
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US-10-192-257-5
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                                                                 Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                             SOFTWARE: PatentIn version 3.1 SEQ ID NO 5
                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 5, Application US/10192257 Publication No. US20030021786A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Hosken, Nancy Ann APPLICANT: Craig H. Day APPLICANT: Davin C. Dillon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 3, Application US/09894998 Patent No. US20020090610A1
                                                                                                                                                                                                                                                                                                                           APPLICANT: Aphton Corporation
TITLE OF INVENTION: Treatment and Prevention of Cancerous and Pre-Cancerous Condit
TITLE OF INVENTION: Liver, Lung and Esophagus
FILE REFERENCE: 1102865-0057
CURRENT APPLICATION NUMBER: US/10/192,257
CURRENT FILING DATE: 2002-07-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: McGowan, Patrick
APPLICANT: Sleath, Paul R.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
TITLE OF INVENTION: TREATMENT OF HERPES SIMPLEX VIRUS INFECTION
FILE REFERENCE: 210121.538
                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: US 60/303,868 PRIOR FILING DATE: 2001-07-09 NUMBER OF SEQ ID NOS: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/894,998
CURRENT FILING DATE: 2001-06-28
NUMBER OF SEQ ID NOS: 64
                                                                                                                                                                                        ORGANISM: Artificial Sequence
                                                                                                                                                                                                              TYPE: PRT
                                                                                                                                                                         FEATURE:
                                                                                                                                                                                                                              LENGTH: 6
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                                                                     Conservative
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Pred. No.
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Pred. No. 2
                                                                     Mismatches
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2.9e+02;
ches 2;
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RESULT 14
US-10-192-257-3
; Sequence 3, Application US/10192257
; Publication No. US20030021786A1
; GENERAL INFORMATION:

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APPLICANT: Aphton Corporation

TITLE OF INVENTION: Treatment and Prevention of Cancerous and Pre-Cancerous Condition

TITLE OF INVENTION: Liver, Lung and Esophagus

FILE REFERENCE: 1102865-0057

CURRENT APPLICATION NUMBER: US/10/192,257

CURRENT FILING DATE: 2002-07-09

PRIOR APPLICATION NUMBER: US 60/303,868

PRIOR APPLICATION NUMBER: US 60/303,868

PRIOR FILING DATE: 2001-07-09

NUMBER OF SEQ ID NOS: 8

SOFTWARE: PATING DATE: 2001-07-09

TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (1). (1)

OTHER INFORMATION: Xaa-pyroglutamic acid
                                                                                                                                                                                                                                       ; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; FEATURE: MISC_FEATURE
; LOCATION: (1)..(1)
; OTHER INFORMATION: Xaa=pyroglutamic acid
US-10-192-257-1
                                                                                                                                        Query Match
Best Local Similarity
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Search completed: February 5, 2003, 09:56:02 Job time: 10.1429 secs
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US-10-192-257-1
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Publication No. US20030021786A1

GENERAL INFORMATION:

APPLICANT: Aphton Corporation

TITLE OF INVENTION: Treatment and Prevention of Cancerous and Pre-Cancerous Condition

TITLE OF INVENTION: Liver, Lung and Esophagus

FILE REFERENCE: 1102865-0057
                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn version 3.1 SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 56.0
Best Local Similarity 100
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/10/192,257
CURRENT FILING DATE: 2002-07-09
PRIOR APPLICATION NUMBER: US 60/303,868
PRIOR FILING DATE: 2001-07-09
NUMBER OF SEQ ID NOS: 8
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4 RPPPPC 9
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100.0%; Pred. No. 1.1e+05;
tive 0; Mismatches 0;
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence:
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75
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: /cgn2_6/ptodata/1/paa/US081_COMB.pep:*
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:/cgn2_6/ptodata/1/paa/US086_COMB.pep:*
:/cgn2_6/ptodata/1/paa/US089_COMB.pep:*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /cgn2_6/ptodata/1/paa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/paa/US06_COMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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56	56	75	75	75	75	Score
74.7	74.7	100.0	100.0	100.0	100.0	Query  Match Length DB ID
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US-08-488-320A-73	PCT-US94-04832A-73	US-09-700-378-5	US-09-700-329-2	PCT-US99-10751-2	PCT-US99-10734-5	DB ID
Sequence 73, Appl	Sequence 73, Appl	Sequence 5, Appli	Sequence 2, Appli	Sequence 2, Appli	Sequence 5, Appli	Description

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10-212-160-47 10-212-160-47 10-212-160-47 10-212-160-47 10-212-160-47 10-22855-96 09-451-320-42 09-99-2855-96 09-924-340-58 09-992-600A-5 09-994-590-489-58 10-000-489-58 10-000-489-58 10-000-305-456-58 60-212-655-59 09-700-335-46-58 09-700-378-2 08-798-423-4 09-700-378-2 08-798-423-4 09-700-378-2 08-798-423-4 09-700-378-2 08-798-423-4 09-700-378-2 09-301-251-25-2 09-305-924-5 09-305-924-5 09-305-924-5 09-305-924-5	T-USO1-14827-1 T-USO1-08656-6 T-USO1-08656-6 S-09-758-444-4
sequence 476, App sequence 476, App sequence 426, App sequence 4290, Ap sequence 4290, Ap sequence 961, App sequence 1548, Appl sequence 58, Appl sequence 58, Appl sequence 58, Appl sequence 58, Appl sequence 58, Appl sequence 2, Appli sequence 2, Appli sequence 2, Appli sequence 2, Appli sequence 2, Appli sequence 20, Appli sequence 20, Appli sequence 218, App sequence 239, App sequence 239, App sequence 2128, App sequence 2128, App sequence 253, Appli sequence 2719, Ap sequence 593, App sequence 5, Appli sequence 3187, Ap sequence 3167, A sequence 3167, A sequence 46904, A	quence 14717, quence 6637, quence 6639, equence 470,

## ALIGNMENTS

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RESULT 1
PCT-US99-10734-5

Sequence 5, Application PC/TUS9910734

GENERAL INFORMATION:
APPLICANT: Gevas, Philip C.
APPLICANT: Gevas, Stephen
APPLICANT: Michaell, Dov
CAPPLICANT: Michaell, Dov
CAPPLICANT: Michaell, Dov
APPLICANT: Michaell, Dov
CAPPLICANT: M
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: LOCATION: (1)
: OTHER INFORMATION: pyroglutamic acid
PCT-US99-10751-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PCT-US99-10751-2
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      Query Match
                                                                                                                                                   SEQ ID NO 2
LENGTH: 12
                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Gevas, Philip
APPLICANT: Grimes, Steph
APPLICANT: Karr, Stephen
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2,
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                                                                                                                                                                                                                                                                             APPLICANT: Watson, Susan TITLE OF INVENTION: Prevention and Treatment of Hypergastrinemia FILE REFERENCE: ACGUSA CURRENT APPLICATION NUMBER: US/09/700,329 CURRENT FILING DATE: 2001-02-08
                                                                                                                                                                                    PRIOR FILING DATE: 1998-05-15
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: PCT/US99/10751
PRIOR FILING DATE: 1999-05-14
PRIOR APPLICATION NUMBER: 60/085,714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: Prevention and Treatment of Hypergastrinemia FILE REFERENCE: 1102865-0035 CURRENT APPLICATION NUMBER: PCT/US99/10751 CURRENT FILING DATE: 1999-05-14 EARLIER APPLICATION NUMBER: US 60/085,714 EARLIER FILING DATE: 1999-05-15 NUMBER OF SEQ ID NOS: 4
                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
                                              FEATURE:
NAME/KEY: MOD_RES
LOCATION: (1)..(1)
OTHER INFORMATION: pyroglutamic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: APHTON CORPORATION
                                                                                                           TYPE: PRT
ORGANISM: human gastrin peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: human or
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ENGTH: 12
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nes 12; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Application US/09700329
                                                                                                                                                                                                                                                                                                                                                                                       Grimes, Stephen
Karr, Stephen
                                                                                                                                                                                                                                                                                                                                                                        Michaeli, Dov
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Pred. No. 0.04;
   Score 75;
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Pred. No. 0.04;
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 DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1;
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Length 12;
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; NAME/KEY: MOD_RES;
; LOCATION: (1)...(1)
; OTHER INFORMATION: pyroglutamic acid
US-09-700-378-5
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PCT-US94-04832A-73
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US-09-700-378-5
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SEQ ID NO 5
LENGTH: 12
TYPE: PRT
ORGANISM: human
                                                                                                                                                                                                                                                                                                                                                                                          Sequence 73, Application PC/TUS9404832A GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 12; Conserva
                                                          STATE: NY
COUNTRY: US
ZIP: 11530
ZIP: 11530
COMPUTER READABLE FORM:
MEDLUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, V6
CURRENT APPLICATION DATA:
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APPLICANT:
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APPLICANT:
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CURRENT FILING DATE: 2000-11-14
PRIOR APPLICATION NUMBER: PT/US99/10734
PRIOR FILING DATE: 1999-05-14
PRIOR FILING DATE: 1998-05-15
PRIOR FILING DATE: 1998-05-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS:
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CLASSIFICATION: ATTORNEY/AGENT INFORMATION
                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Immunogenic LHRH peptide constructs
TITLE OF INVENTION: and synthetic universal immune stimulators
NUMBER OF SEQUENCES: 114
                                                                                                                                                                                                                                                                                                                                   APPLICANT: Ladd, Anna
APPLICANT: Wang, Chang Yi
APPLICANT: Zamb, Timothy
                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
                               APPLICATION NUMBER: FILING DATE: 13-AP
                                                                                                                                                                                                                      STREET: 400 Garden City
                                                                                                                                                                                                                                                         ADDRESSEE:
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                                                                                                                                                                                                                                      400 Garden City Plaza
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                                 13-APR-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Method for the Treatment of Gastroesophageal Reflux Disease
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                                                                                   Version #1.25
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Best Local Similarity 81.8
""" onservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (516)742-4366
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
                                                                             INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                      CLASSIFATION DATA:
PRIOR APPLICATION NUMBER: 08/48
PTILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: Immunogenic Peptides Which Contain LHRH
TITLE OF INVENTION: And A Helper T-Cell Epitope For Treatment Of Prostate Cancer
TITLE OF INVENTION: And Induction Of Infertility
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: li
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (516)742-4343
                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 114
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN
                           SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
                                                                                                         REFERENCE/DOCKET NUMBER: 11
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)758-4800
TELEFAX: (212)751-6849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
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                                                                                                                                                                                                                APPLICATION NUMBER: 08/446
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: 08/229
FILING DATE: 14-APR-1994
APPLICATION NUMBER: 08/057
FILING DATE: 27-APR-1993
 MOLECULE TYPE:
                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: NEW YORK
STATE: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 07
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET:
                 TOPOLOGY:
                                                                                                                                                                      NAME: Maria C. H. L
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
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                                             11 amino acids
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Zamb, Timothy
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IBM PC compatible
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peptide
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81.8%;
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                                                                                                                                                                                                                                  08/057,166
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PCT-US01-14827-14717

; Sequence 14717, Application PC/TUS0114827
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; ITTLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POI
; TITLE REFERENCE: 21272-104
; CURRENT APPLICATION NUMBER: PCT/US01/14827
; CURRENT FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: 09/577,408
; PRIOR FILING DATE: 2000-05-18
; PRIOR FILING DATE: 2000-05-18
; PRIOR FILING DATE: 1000-18
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                   Query Match
Best Local Similarity
"---hes 8; Conserv?
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Ωy
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                                                                                                      PCT-US01-08656-6637
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Best Local Similarity 81.1
Matches 9; Conservative
                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 10994
SOFTWARE: CLUSTOM
SEQ ID NO 6637
LENGTH: 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 6637, Application PC/TUS0108656 GENERAL INFORMATION:
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SEQ ID NO 14717
LENGTH: 160
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Best Local
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TITLE OF INVENTION: NOVEL MACROPHAGE NUCLEIC ACIDS AND POLYPEPTIDES
FILE REFERENCE: 21272-066
                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: 09/770,160 PRIOR FILING DATE: 2001-01-26
                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: 09/522,929 PRIOR FILING DATE: 2000-04-18
                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: PCT/US01/08656
CURRENT FILING DATE: 2001-04-16
                                                                                                                    NAME/KEY: misc_feature
LOCATION: (1)...(139)
OTHER INFORMATION: Xaa = X or * as defined in Table 2
                                                                                                                                                                    FEATURE:
                                                                                                                                                                                     ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Homo sapiens
                                                                                                                                                                                                          TYPE: PRT
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1 ELGPQGRPPPP
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81.8%;
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Pred.
                                                  Score 55; DB
Pred. No. 88;
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                                   Mismatches
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6.7;
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Sequence 6639, Application PC/TUS0108656
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICATION INFORMATION:
FILLE OF INVENTION: NOVEL MACROPHAGE NUCLEIC AC:
FILE REFERENCE: 21272-066
CURRENT APPLICATION NUMBER: PCT/US01/08656
CURRENT FILLING DATE: 2001-04-16
PRIOR APPLICATION NUMBER: 09/522,929
PRIOR APPLICATION NUMBER: 09/770,160
PRIOR APPLICATION NUMBER: 09/770,160
PRIOR APPLICATION NUMBER: 09/770,160
PRIOR APPLICATION NUMBER: 09/770,160
PRIOR FILING DATE: 2001-01-26
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Best Local S
Matches 8
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PRIOR APPLICATION NUMBER: 60/180,628
PRIOR FILING DATE: 2000-02-04
NUMBER OF SEQ ID NOS: 638
SOFFWARE: Patentin Ver. 2.0
SEQ ID NO 470
LENGTH: 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 470, Application US/09758444
GENERAL INFORMATION:
APPLICANT: Rosen et al.
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SOFTWARE: Custom
SEQ ID NO 6639
LENGTH: 169
TYPE: PRT
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CURRENT FILING DATE: 2001-01-11
                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: Nucleic Acids, Proteins, FILE REFERENCE: PM032
                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Homo :
FEATURE:
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                                                                                                                                       NAME/KEY: SITE LOCATION: (73) OTHER INFORMATION:
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                                                LOCATION: (75)
OTHER INFORMATION:
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Best Local
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LENGTH: 323
TYPE: PRT
ORGANISM: Homo sapiens
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Best Local
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PRIOR APPLICATION NUMBER: 60/179,065
PRIOR FILING DATE: 2000-01-31
PRIOR APPLICATION NUMBER: 60/180,628
PRIOR FILING DATE: 2000-02-04
NUMBER OF SEQ ID NOS: 638
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CURRENT FILING DATE: 2001-01-11
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                                                                                                                                                      LOCATION: (293)
OTHER INFORMATION:
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LOCATION: (319)
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OTHER INFORMATION:
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NAME/KEY: SITE
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Pred. No.
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RESULT 12 US-10-212-160-476

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US-10-015-127-10407; Sequence 10407, Application US/10015127; GENERAL INFORMATION:
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SEQ ID NO 476
LENGTH: 323
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                         APPLICANT: Bower, Stanley G.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
TITLE OF INVENTION: Sphingomonas elodea genome sequences
FILE REFERENCE: 38-10(15806)B
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NUMBER OF SEQ ID NOS: 638
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PRIOR APPLICATION NUMBER: 60/179,065
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CURRENT FILING DATE:
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ORGANISM: Homo sapiens
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OTHER INFORMATION: Xaa
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              APPLICATION NUMBER:
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; ORGANISM: Sphingomonas elodea US-10-015-127-10407
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai
APPLICANT: CHEN, Xianfeng
APPLICANT: SUBRAMANIAN, Gopalakrishnan
APPLICANT: SHENG, Liansheng
APPLICANT: SHENG, Liansheng
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS 42-59,
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS 42-59,
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS 42-59,
TITLE OF INVENTION: SUBJECT OF STREET 
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Matches 9
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CURRENT FILING DATE: 1999-10-05
NUMBER OF SEQ ID NOS: 3978
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 962
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 962, Application PC/TUS9922855 GENERAL INFORMATION: APPLICANT: Ceres, Inc.
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LENGTH: 172
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SOFTWARE: PatentIn Ve
SEQ ID NO 4290
LENGTH: 222
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                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/451,320 CURRENT FILING DATE: 1999-12-01 NUMBER OF SEQ ID NOS: 6998
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                                                                                                                            OTHER INFORMATION: any n or Xaa
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Pred. No. 2.7e+02;
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Pred. No. 2
Score 51; DB 18;
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GenCore version (c) 1993 - 2003

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Result
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ALIGNMENTS	50	50	50	50	50	50	50	50	50	50	50	50	50	50	50	50	50	50	50
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	Sequence 88529,	Sequence 88524,	Sequence 88520,	•	•	•	•	Sequence 88528,	•	,	•	•	`	`	•	2,	Sequence 88518, ,	-	Sequence 88537,
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#### Query Match Best Local Similarity Theches 12; Conserve ; NAME/KEY: MOD\_RES; LOCATION: (1)..(1); OTHER INFORMATION: pyroglutamic acid US-10-314-057-5 RESULT 2 US-10-154-678-58 RESULT 1 US-10-314-057-5 Вb Ω CURRENT APPLICATION NUMBER: US/10/314,057 CURRENT FILING DATE: 2002-12-06 PRIOR APPLICATION NUMBER: US/09/700,378 PRIOR FILING DATE: 2000-11-14 PRIOR APPLICATION NUMBER: PCT/US99/10734 PRIOR FILING DATE: 1999-05-14 PRIOR APPLICATION NUMBER: 60/085,610 PRIOR APPLICATION NUMBER: 60/085,610 PRIOR FILING DATE: 1998-05-15 Sequence 58, Application US/10154678 GENERAL INFORMATION: NUMBER OF SEQ ID NOS: 8 SOFTWARE: PatentIn version SEQ ID NO 5 LENGTH: 12 Sequence 5, Application US/10314057 GENERAL INFORMATION: APPLICANT: Benjanin, Stephane APPLICANT: Tanaka, Hiroaki TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF FILE REFERENCE: 182.US1.REG CURRENT APPLICATION NUMBER: US/10/154,678 CURRENT FILING DATE: 2002-10-15 APPLICANT: Gevas, Philip APPLICANT: Stephen, Grimes APPLICANT: Karr, Stephen APPLICANT: Michaeli, Dov TITLE OF INVENTION: Method for the Treatment of Gastroesophageal Reflux Disease FILE REFERENCE: ACGIUSA TYPE: PRT ORGANISM: human FEATURE: 1 ELGPQGRPPPPC 12 ||||||||||| 1 ELGPQGRPPPPC 12 100.0%; ilarity 100.0%; Conservative 0 0, Score 75; I Mismatches DB 6; .0038; Length 12; Indels 0,: Gaps 0;

Sequence

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US-09-724-676A-88534
; Sequence 88534, Application US/09724676A
; GENERAL INFORMATION:
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; SEQ ID NO 88534
; LENGTH: 265
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-676-88534
                                                               ; ORGANISM: Homo sapiens US-09-724-676A-88534
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PRIOR FILING DATE: 2001-07-13
PRIOR APPLICATION NUMBER: US 60/302,277
PRIOR FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: US 60/298,698
PRIOR FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: US 60/293,574
PRIOR FILING DATE: 2001-05-25
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GENERAL INFORMATION:
APPLICAMT: Compugen LTD
TITLE OF INVENTION: Variants of alternative
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
                                                                                                             SOFTWARE: PatentIn version 3.2 SEQ ID NO 88534 LENGTH: 265
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LENGTH: 163
                               Query Match
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APPLICANT: Compugen LTD
ITILE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676
CURRENT FILLING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: PatentIn version 3.2
SEQ ID NO 88523
LENGTH: 319
TYPE: PRT
ORGANISM: Homo sapiens
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US-09-724-676-88527
US-09-724-676-88527, Application US/09724676
; GENERAL INFORMATION:
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Best Local Similarity
Thehes 8; Conserv.
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US-09-724-676-88523
US-09-724-676-88523, Application US/09724676
GENERAL INFORMATION:
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US-09-724-676-88519
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SEQ ID NO 88519
LENCTH: 319
TYPE: PRT
                    SOFTWARE: PatentIn version 3.2
SEQ ID NO 88527
LENGTH: 319
TYPE: PRT
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ITILE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
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                                                                                    FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
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ORGANISM: Homo sapiens
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US-09-724-676-88539
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US-09-724-676-88532
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APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: Patentin version 3.2
SEQ ID NO 88535
LENGTH: 319
                                                                                                Sequence 88539, Application US/09724676 GENERAL INFORMATION:
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SOFTWARE: PatentIn version 3.2
SEQ ID NO 88532
LENGTH: 319
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APPLICANT: Compugen LTD TITLE OF INVENTION: Variants of alternative splicing FILE REFERENCE: 129181.4 Compugen CURRENT APPLICATION NUMBER: US/09/724,676 CURRENT FILING DATE: 2000-11-28 NUMBER OF SEQ ID NOS: 97222
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TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676
CCURRENT FILING DATE: 2000-11-28
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RESULT 13
US-09-724-676A-88527
; Sequence 88527, Application US/09724676A
; GENERAL INFORMATION:
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US-09-724-676A-88523
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SOFTWARE: Patentin version 3.2
SEQ ID NO 88523
LENGTH: 319
TYPDE: Parent
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US-09-724-676A-88519
; Sequence 88519, Application US/09724676A
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SEQ ID NO 88519
LENGTH: 319
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SEQ ID NO 88539
LENCTH: 319
TYPE: PRT
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TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676A
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
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TYPE: PRT
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APPLICANT: Compugen LTD

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RESULT 15
US-09-724-676A-88535
US-09-724-676A-88535, Application US/09724676A
Sequence 88535, Application US/09724676A
GENERAL INFORMATION:
APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative splicing
EILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676A
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: Patentin version 3.2
SEQ ID NO 88535
LENGTH: 319
TYPE: PRT
ORGANISM: Homo sapiens
US-09-724-676A-88535
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US-09-724-676A-88532
; Sequence 88532, Application US/09724676A
; GENERAL INFORMATION:
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; ORGANISM: Homo sapiens
US-09-724-676A-88527
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Best Local S
Matches 8
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TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676A
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: PatentIn version 3.2
SEQ ID NO 88532
LENGTH: 319
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Best Local Similarity 88.9
Matches 8; Conservative
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Search completed: February 5, 2003, 09:50:58 Job time: 19.4286 secs